

32600PWO.ST25.txt
SEQUENCE LISTING

<110> DeveloGen Aktiengesellschaft für entwicklungsbiologische
Forschung

<120> Use of secreted protein products for preventing and treating
pancreatic diseases and/or obesity and/or metabolic syndrome

<130> 32600PWO

<140> PCT/EP2005/001711
<141> 2005-02-18

<150> EP04003914.1
<151> 2004-02-20

<160> 61

<170> PatentIn version 3.3

<210> 1
<211> 19
<212> DNA
<213> Artificial

<220>
<223> Artificial Sequence

<220>
<221> misc_feature
<223> Primer: Mouse SF02 forward primer

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cggacagcat cagccttga 19

<210> 2
<211> 20
<212> DNA
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<220>
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<221> misc_feature
<223> Primer: Mouse SF02 reverse primer

<400> 2
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<210> 3
<211> 19
<212> DNA
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<223> Taqman probe: Mouse SF02 Taqman probe

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ctgcgcaaac cgcacggca

19

<210> 4
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 <212> DNA
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 <223> Primer: Mouse SF03 forward primer

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19

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<220>
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<220>
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 <223> Primer: Mouse SF03 reverse primer

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22

<210> 6
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<220>
 <223> Artificial Sequence

<220>
 <221> misc_feature
 <223> Tagman probe: Mouse SF03 Tagman probe

<400> 6
 acaccaacgc catgttcaag aataactacc c

31

<210> 7
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 <213> Artificial

<220>
 <223> Artificial Sequence

<220>
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 <223> Primer: Mouse SF04 forward primer

<400> 7

ggtacaacct ggcggtgg

18

<210> 8

<211> 23

<212> DNA

<213> Artificial

<220>

<223> Artificial Sequence

<220>

<221> misc_feature

<223> Primer: Mouse SF04 reverse primer

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<210> 9

<211> 18

<212> DNA

<213> Artificial

<220>

<223> Artificial Sequence

<220>

<221> misc_feature

<223> Taqman probe: Mouse SF04 Taqman probe

<400> 9

tgcccgtggc tgagccgc

18

<210> 10

<211> 1285

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (514)..(1131)

<223> SF01, cDNA: NM_026161, Protein: NP_080437

<400> 10

ggtggtcccc actcgtcgcc ggctaaaccc ccgccacccc tggaggcccg gtcaagccgc 60

agcgcgggcg accagtgtgt agcccggcgt cctcaccgag caggatagcc ggctgggacc 120

gaagccgacc cgcccgccac cagccaggtg ccatgctgct gctcttgctg ggcttcctag 180

gcccggcggc ctgctgggca ctgggcccgg ctggccctgg ctctcggag ctgcggtcag 240

ccttctcggc ggctcgcacc acccgcgtgg agggcacgtc ggagatggcg gtgaccttcg 300

acaaggtgta cgtgaacatc gggggtgact tcgacgcagc caccgggcgg ttccgctgtc 360

gcgtgccggg cgctacttc ttctccttca cggccggcaa ggccgcaca agagcctgtc 420

ggtgatgctg gtgcgcaacc gcgacgaggt gcaggcgctg gctttcgacg agcagcgacg 480

gccaggcgcg cggcgcgcgc cagccagagc gcc atg ctg cag ctc gac tac ggc 534

Met Leu Gln Leu Asp Tyr Gly
1 5

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gac acg gtg tgg ctg cgg ctg cac ggc gct ccg cag tac gcg ctc ggc 582
 Asp Thr Val Trp Leu Arg Leu His Gly Ala Pro Gln Tyr Ala Leu Gly
 10 15 20

gcg ccg ggc gcc acc ttc agc ggc tac ctg gtg tac gcg gac gcc gac 630
 Ala Pro Gly Ala Thr Phe Ser Gly Tyr Leu Val Tyr Ala Asp Ala Asp
 25 30 35

gcc gac gcg cct gcg cgc ggc ccc gcg gcc ccg gag ccg cgc tcg gcc 678
 Ala Asp Ala Pro Ala Arg Gly Pro Ala Ala Pro Glu Pro Arg Ser Ala
 40 45 50 55

ttc tcc gcg gcg cgc acg cgc agc ctg gtg ggc tcg gac gcc gcc ccc 726
 Phe Ser Ala Ala Arg Thr Arg Ser Leu Val Gly Ser Asp Ala Ala Pro
 60 65 70

ggc ccg cgc cac cgg ccg ttg gcc ttc gac acc gag ctg gta aac ata 774
 Gly Pro Arg His Arg Pro Leu Ala Phe Asp Thr Glu Leu Val Asn Ile
 75 80 85

ggt ggc gac ttc gac gcg gcg gcc ggc gtg ttc cgc tgc cgc ctg ccg 822
 Gly Gly Asp Phe Asp Ala Ala Ala Gly Val Phe Arg Cys Arg Leu Pro
 90 95 100

gga gcc tat ttc ttc tcc ttc acg ctg ggc aag ctg ccg cgc aag acg 870
 Gly Ala Tyr Phe Phe Ser Phe Thr Leu Gly Lys Leu Pro Arg Lys Thr
 105 110 115

ctg tcg gtg aag ctg atg aag aac cgc gac gag gtg cag gcc atg att 918
 Leu Ser Val Lys Leu Met Lys Asn Arg Asp Glu Val Gln Ala Met Ile
 120 125 130 135

tac gac gac ggc gct tcg agg cgc cgt gag atg cag agt cag agc gtg 966
 Tyr Asp Asp Gly Ala Ser Arg Arg Arg Glu Met Gln Ser Gln Ser Val
 140 145 150

agg ctg ccg ctg cgg cgc ggc gac gcc gtc tgg cta ctt agc cac gat 1014
 Arg Leu Pro Leu Arg Arg Gly Asp Ala Val Trp Leu Leu Ser His Asp
 155 160 165

cac gat ggc tat ggc gcc tac agc aac cac ggc aag tac atc act ttc 1062
 His Asp Gly Tyr Gly Ala Tyr Ser Asn His Gly Lys Tyr Ile Thr Phe
 170 175 180

tca ggc ttc ctg gtg tac cct gac ctc gcc gcc gcc ggc ccg ccg gcc 1110
 Ser Gly Phe Leu Val Tyr Pro Asp Leu Ala Ala Ala Gly Pro Pro Ala
 185 190 195

ctc aag ccc cca gag ctc tga gcctctgctt ggaggagccc gggagagccg 1161
 Leu Lys Pro Pro Glu Leu
 200 205

tggggcatgc atgccgagcc gggaccgcgg cccgaacgcc ccaccggtcc gagcatgact 1221

gcctgctcag cagcctgga ctctgccaat aaagtggggc tgcctgtcag ccttatggtc 1281

ctgc 1285

<210> 11
 <211> 205
 <212> PRT
 <213> Mus musculus
 <400> 11

Met Leu Gln Leu Asp Tyr Gly Asp Thr Val Trp Leu Arg Leu His Gly

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1              5              10              15
Ala Pro Gln Tyr Ala Leu Gly Ala Pro Gly Ala Thr Phe Ser Gly Tyr
      20              25              30
Leu Val Tyr Ala Asp Ala Asp Ala Asp Ala Pro Ala Arg Gly Pro Ala
      35              40              45
Ala Pro Glu Pro Arg Ser Ala Phe Ser Ala Ala Arg Thr Arg Ser Leu
      50              55              60
Val Gly Ser Asp Ala Ala Pro Gly Pro Arg His Arg Pro Leu Ala Phe
      65              70              75              80
Asp Thr Glu Leu Val Asn Ile Gly Gly Asp Phe Asp Ala Ala Ala Gly
      85              90              95
Val Phe Arg Cys Arg Leu Pro Gly Ala Tyr Phe Phe Ser Phe Thr Leu
      100             105             110
Gly Lys Leu Pro Arg Lys Thr Leu Ser Val Lys Leu Met Lys Asn Arg
      115             120             125
Asp Glu Val Gln Ala Met Ile Tyr Asp Asp Gly Ala Ser Arg Arg Arg
      130             135             140
Glu Met Gln Ser Gln Ser Val Arg Leu Pro Leu Arg Arg Gly Asp Ala
      145             150             155             160
Val Trp Leu Leu Ser His Asp His Asp Gly Tyr Gly Ala Tyr Ser Asn
      165             170             175
His Gly Lys Tyr Ile Thr Phe Ser Gly Phe Leu Val Tyr Pro Asp Leu
      180             185             190
Ala Ala Ala Gly Pro Pro Ala Leu Lys Pro Pro Glu Leu
      195             200             205

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<210> 12
<211> 1393
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (225)..(1214)
<223> SF01, cDNA: NM_031909, Protein: NP_114115

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<400> 12
gaattcggca cgaggcgccc ggcccctggc cccagcaccc tgtccgctgc cgcctcagag      60
ccgggaaaag cagccggagc ccccgccgcc cctgccgcag cgcgggcggt cagcgcgcag      120
cccggcaccc gcagcctgca gcctgcagcc cgcagcccg cagccggagc cagatcgcg      180

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gctcagaccg aacccgactc gaccgcccgc cccagccagg cgcc atg ctg ccg ctt 236
Met Leu Pro Leu
1

ctg ctg ggc ctg ctg ggc cca gcg gcc tgc tgg gcc ctg ggc ccg acc 284
Leu Leu Gly Leu Leu Gly Pro Ala Ala Cys Trp Ala Leu Gly Pro Thr
5 10 15 20

ccc ggc ccg gga tcc tct gag ctg cgc tcg gcc ttc tcg gcg gca cgc 332
Pro Gly Pro Gly Ser Ser Glu Leu Arg Ser Ala Phe Ser Ala Ala Arg
25 30 35

acc acc ccc ctg gag ggc acg tcg gag atg gcg gtg acc ttc gac aag 380
Thr Thr Pro Leu Glu Gly Thr Ser Glu Met Ala Val Thr Phe Asp Lys
40 45 50

gtg tac gtg aac atc ggg ggc gac ttc gat gtg gcc acc ggc cag ttt 428
Val Tyr Val Asn Ile Gly Gly Asp Phe Asp Val Ala Thr Gly Gln Phe
55 60 65

cgc tgc cgc gtg ccc ggc gcc tac ttc ttc tcc ttc acg gct ggc aag 476
Arg Cys Arg Val Pro Gly Ala Tyr Phe Phe Ser Phe Thr Ala Gly Lys
70 75 80

gcc ccg cac aag agc ctg tcg gtg atg ctg gtg cga aac cgc gac gag 524
Ala Pro His Lys Ser Leu Ser Val Met Leu Val Arg Asn Arg Asp Glu
85 90 95 100

gtg cag gcg ctg gcc ttc gac gag cag cgg cgg cca ggc gcg cgg cgc 572
Val Gln Ala Leu Ala Phe Asp Glu Gln Arg Arg Pro Gly Ala Arg Arg
105 110 115

gca gcc agc cag agc gcc atg ctg cag ctc gac tac ggc gac aca gtg 620
Ala Ala Ser Gln Ser Ala Met Leu Gln Leu Asp Tyr Gly Asp Thr Val
120 125 130

tgg ctg cgg ctg cat ggc gcc ccg cac tac gcg cta ggc gcg ccc ggc 668
Trp Leu Arg Leu His Gly Ala Pro His Tyr Ala Leu Gly Ala Pro Gly
135 140 145

gcc acc ttc agc ggc tac cta gtc tac gcc gac gcc gac gct gac gcg 716
Ala Thr Phe Ser Gly Tyr Leu Val Tyr Ala Asp Ala Asp Ala Asp Ala
150 155 160

cct gcg cgc ggg ccg ccc gcg ccc ccc gag ccg cgc tcg gcc ttc tcg 764
Pro Ala Arg Gly Pro Pro Ala Pro Pro Glu Pro Arg Ser Ala Phe Ser
165 170 175 180

gcg gcg cgc acg cgc agc ttg gtg ggc tcg gac gct ggc ccc ggg ccg 812
Ala Ala Arg Thr Arg Ser Leu Val Gly Ser Asp Ala Gly Pro Gly Pro
185 190 195

cgg cac caa cca ctc gcc ttc gac acc gag ttc gtc aac att ggc ggc 860
Arg His Gln Pro Leu Ala Phe Asp Thr Glu Phe Val Asn Ile Gly Gly
200 205 210

gac ttc gac gcg gcg gcc ggc gtg ttc cgc tgc cgt ctg ccc ggc gcc 908
Asp Phe Asp Ala Ala Ala Gly Val Phe Arg Cys Arg Leu Pro Gly Ala
215 220 225

tac ttc ttc tcc ttc acg ctg ggc aag ctg ccg cgt aag acg ctg tcg 956
Tyr Phe Phe Ser Phe Thr Leu Gly Lys Leu Pro Arg Lys Thr Leu Ser
230 235 240

gtt aag ctg atg aag aac cgc gac gag gtg cag gcc atg att tac gac 1004
Val Lys Leu Met Lys Asn Arg Asp Glu Val Gln Ala Met Ile Tyr Asp
245 250 255 260

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gac ggc gcg tcg cgg cgc cgc gag atg cag agc cag agc gtg atg ctg      1052
Asp Gly Ala Ser Arg Arg Arg Glu Met Gln Ser Gln Ser Val Met Leu
                265                270                275

gcc ctg cgg cgc ggc gac gcc gtc tgg ctg ctc agc cac gac cac gac      1100
Ala Leu Arg Arg Gly Asp Ala Val Trp Leu Leu Ser His Asp His Asp
                280                285                290

ggc tac ggc gcc tac agc aac cac ggc aag tac atc acc ttc tcc ggc      1148
Gly Tyr Gly Ala Tyr Ser Asn His Gly Lys Tyr Ile Thr Phe Ser Gly
                295                300                305

ttc ctg gtg tac ccc gac ctc gcc ccc gcc gcc ccg ccg ggc ctc ggg      1196
Phe Leu Val Tyr Pro Asp Leu Ala Pro Ala Ala Pro Pro Gly Leu Gly
                310                315                320

gcc tcg gag cta ctg tga gccccggggc agagaagagc ccgggagggc          1244
Ala Ser Glu Leu Leu
325

cagggggcgtg catgccaggc cgggcccagag gctcgaaagt cccgcgcgag cgccacggcc 1304
tccggggcgcg cctggactct gccataaag cggaaagcgg gcacgcgcag cgcccggcag 1364
cccaggcaaa aaaaaaaaaa aaaaaaaaaa          1393

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<210> 13
<211> 329
<212> PRT
<213> Homo sapiens

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<400> 13
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Met Leu Pro Leu Leu Leu Gly Leu Leu Gly Pro Ala Ala Cys Trp Ala
1                5                10                15

Leu Gly Pro Thr Pro Gly Pro Gly Ser Ser Glu Leu Arg Ser Ala Phe
                20                25                30

Ser Ala Ala Arg Thr Thr Pro Leu Glu Gly Thr Ser Glu Met Ala Val
                35                40                45

Thr Phe Asp Lys Val Tyr Val Asn Ile Gly Gly Asp Phe Asp Val Ala
50                55                60

Thr Gly Gln Phe Arg Cys Arg Val Pro Gly Ala Tyr Phe Phe Ser Phe
65                70                75                80

Thr Ala Gly Lys Ala Pro His Lys Ser Leu Ser Val Met Leu Val Arg
                85                90                95

Asn Arg Asp Glu Val Gln Ala Leu Ala Phe Asp Glu Gln Arg Arg Pro
100                105                110

Gly Ala Arg Arg Ala Ala Ser Gln Ser Ala Met Leu Gln Leu Asp Tyr
115                120                125

Gly Asp Thr Val Trp Leu Arg Leu His Gly Ala Pro His Tyr Ala Leu

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130

135

140

Gly Ala Pro Gly Ala Thr Phe Ser Gly Tyr Leu Val Tyr Ala Asp Ala
 145 150 155 160

Asp Ala Asp Ala Pro Ala Arg Gly Pro Pro Ala Pro Pro Glu Pro Arg
 165 170 175

Ser Ala Phe Ser Ala Ala Arg Thr Arg Ser Leu Val Gly Ser Asp Ala
 180 185 190

Gly Pro Gly Pro Arg His Gln Pro Leu Ala Phe Asp Thr Glu Phe Val
 195 200 205

Asn Ile Gly Gly Asp Phe Asp Ala Ala Ala Gly Val Phe Arg Cys Arg
 210 215 220

Leu Pro Gly Ala Tyr Phe Phe Ser Phe Thr Leu Gly Lys Leu Pro Arg
 225 230 235 240

Lys Thr Leu Ser Val Lys Leu Met Lys Asn Arg Asp Glu Val Gln Ala
 245 250 255

Met Ile Tyr Asp Asp Gly Ala Ser Arg Arg Arg Glu Met Gln Ser Gln
 260 265 270

Ser Val Met Leu Ala Leu Arg Arg Gly Asp Ala Val Trp Leu Leu Ser
 275 280 285

His Asp His Asp Gly Tyr Gly Ala Tyr Ser Asn His Gly Lys Tyr Ile
 290 295 300

Thr Phe Ser Gly Phe Leu Val Tyr Pro Asp Leu Ala Pro Ala Ala Pro
 305 310 315 320

Pro Gly Leu Gly Ala Ser Glu Leu Leu
 325

<210> 14
 <211> 2388
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (244)..(1092)
 <223> SF02, cDNA: NM_178644, Protein: NP_848759

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 actcgggggtg cgtgggtgta cgcgggccac gtgaattcgc tgcacgtcgt ggggaacctc 120
 cgggttgagt ctcccctcta gaagtagggg actgccggga atccccgaac cggacccccca 180

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acttcgagca aactttttagt ggcggtctcc cctccccccac gcggcgcgcc gggggccccg	240
ggg atg cgg ccc cct ggc tgc cgc gac gtc ccc tcg gcg cgc ccc gcg Met Arg Pro Pro Gly Cys Arg Asp Val Pro Ser Ala Arg Pro Ala 1 5 10 15	288
ctg ccg ctg ctg ctg ctg ctg ctg tcg ccg ctg ctg ctt ggg gcg ctg Leu Pro Leu Leu Leu Leu Leu Leu Ser Pro Leu Leu Leu Gly Ala Leu 20 25 30	336
cac ggc gtg ggc gcg ggc agc ggc gct ccg gcc gag ctg cgg gtc cga His Gly Val Gly Ala Gly Ser Gly Ala Pro Ala Glu Leu Arg Val Arg 35 40 45	384
gtg aga ctg ccc gac agc cag gtg atc gag gag agt cta cag gcg gac Val Arg Leu Pro Asp Ser Gln Val Ile Glu Glu Ser Leu Gln Ala Asp 50 55 60	432
agc gac gcg gac agc atc agc ctt gat ctg cgc aaa ccc gac ggc act Ser Asp Ala Asp Ser Ile Ser Leu Asp Leu Arg Lys Pro Asp Gly Thr 65 70 75	480
ctc atc tcc ttc atc gcg gat ttc aag aag gac gtg aag atc ttc cga Leu Ile Ser Phe Ile Ala Asp Phe Lys Lys Asp Val Lys Ile Phe Arg 80 85 90 95	528
gcc ctg atc ctc ggg gag ctg gag aag ggg cag agt cag ttc cag gca Ala Leu Ile Leu Gly Glu Leu Glu Lys Gly Gln Ser Gln Phe Gln Ala 100 105 110	576
ctt tgc ttt gtc aca agg ctg cac cac aat gac atc atc ccc agt gag Leu Cys Phe Val Thr Arg Leu His His Asn Asp Ile Ile Pro Ser Glu 115 120 125	624
gcc atg gcc aag ctc cgg cag aaa aac ccc cgc gca gtg cgg cag gct Ala Met Ala Lys Leu Arg Gln Lys Asn Pro Arg Ala Val Arg Gln Ala 130 135 140	672
gag gaa gtg agg ggt ctg gaa cag tta cat atg gat atc gct gtt aac Glu Glu Val Arg Gly Leu Glu Gln Leu His Met Asp Ile Ala Val Asn 145 150 155	720
ttc agc cag ggg ggc ctg ctg agt ccc cat ctc cac aac gta tgt gct Phe Ser Gln Gly Gly Leu Leu Ser Pro His Leu His Asn Val Cys Ala 160 165 170 175	768
gag gcc aca gat gcc atc tac acc cgc cag gag gat gtc cag ttc tgg Glu Ala Thr Asp Ala Ile Tyr Thr Arg Gln Glu Asp Val Gln Phe Trp 180 185 190	816
aca gag cga ggt gtg gac agt tct gtt ttc gag gct ctg ccc aag gca Thr Glu Arg Gly Val Asp Ser Ser Val Phe Glu Ala Leu Pro Lys Ala 195 200 205	864
tta gaa cag gcg gaa tta cct cgt tgt gga cga gtt ggg gat cga gga Leu Glu Gln Ala Glu Leu Pro Arg Cys Gly Arg Val Gly Asp Arg Gly 210 215 220	912
aag ccc tgt act tgc cac tac agt ctg agc ctg gcc tgg tac cca tgc Lys Pro Cys Thr Cys His Tyr Ser Leu Ser Leu Ala Trp Tyr Pro Cys 225 230 235	960
atg ctc aag tat tgc cac agt cgt gat cgg cca gcg ccc tac aag tgt Met Leu Lys Tyr Cys His Ser Arg Asp Arg Pro Ala Pro Tyr Lys Cys 240 245 250 255	1008
ggc atc cga agc tgc agg aaa agc tac acc ttt gac ttc tat gta cct	1056

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Gly Ile Arg Ser Cys Arg Lys Ser Tyr Thr Phe Asp Phe Tyr Val Pro
260 265 270

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<210> 15
<211> 282
<212> PRT
<213> Mus musculus
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Met Arg Pro Pro Gly Cys Arg Asp Val Pro Ser Ala Arg Pro Ala Leu
1 5 10 15

Gly Val Gly Ala Gly Ser Gly Ala Pro Ala Glu Leu Arg Val Arg Val
10

35

40

45

Arg Leu Pro Asp Ser Gln Val Ile Glu Glu Ser Leu Gln Ala Asp Ser
50 55 60

Asp Ala Asp Ser Ile Ser Leu Asp Leu Arg Lys Pro Asp Gly Thr Leu
65 70 75 80

Ile Ser Phe Ile Ala Asp Phe Lys Lys Asp Val Lys Ile Phe Arg Ala
85 90 95

Leu Ile Leu Gly Glu Leu Glu Lys Gly Gln Ser Gln Phe Gln Ala Leu
100 105 110

Cys Phe Val Thr Arg Leu His His Asn Asp Ile Ile Pro Ser Glu Ala
115 120 125

Met Ala Lys Leu Arg Gln Lys Asn Pro Arg Ala Val Arg Gln Ala Glu
130 135 140

Glu Val Arg Gly Leu Glu Gln Leu His Met Asp Ile Ala Val Asn Phe
145 150 155 160

Ser Gln Gly Gly Leu Leu Ser Pro His Leu His Asn Val Cys Ala Glu
165 170 175

Ala Thr Asp Ala Ile Tyr Thr Arg Gln Glu Asp Val Gln Phe Trp Thr
180 185 190

Glu Arg Gly Val Asp Ser Ser Val Phe Glu Ala Leu Pro Lys Ala Leu
195 200 205

Glu Gln Ala Glu Leu Pro Arg Cys Gly Arg Val Gly Asp Arg Gly Lys
210 215 220

Pro Cys Thr Cys His Tyr Ser Leu Ser Leu Ala Trp Tyr Pro Cys Met
225 230 235 240

Leu Lys Tyr Cys His Ser Arg Asp Arg Pro Ala Pro Tyr Lys Cys Gly
245 250 255

Ile Arg Ser Cys Arg Lys Ser Tyr Thr Phe Asp Phe Tyr Val Pro Gln
260 265 270

Lys Gln Leu Cys Leu Trp Asp Glu Asp Pro
275 280

<210> 16
<211> 1957
<212> DNA
<213> Homo sapiens

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<220>

<221> CDS

<222> (242)..(1063)

<223> SF02, cDNA: NM_178507, Protein: NP_848602

<400> 16

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cccccgggcg agcggctccc gggcgccccg aactagcccc caactttggg cgaagtttgc      180
ctgcgcctct ccccgcccc acgcggcgcg ccggggccgc ggacggcagc ggccccggg      240
g atg cgc ctt ccc ggg gta ccc ctg gcg cgc cct gcg ctg ctg ctg ctg      289
Met Arg Leu Pro Gly Val Pro Leu Ala Arg Pro Ala Leu Leu Leu Leu
  1          5          10          15

ctg ccg ctg ctc gcg ccg ctg ctg gga acg ggt gcg ccg gcc gag ctg      337
Leu Pro Leu Leu Ala Pro Leu Leu Gly Thr Gly Ala Pro Ala Glu Leu
          20          25          30

cgg gtc cgc gtg cgg ctg ccg gac ggc cag gtg acc gag gag agc ctg      385
Arg Val Arg Val Arg Leu Pro Asp Gly Gln Val Thr Glu Glu Ser Leu
          35          40          45

cag gcg gac agc gac gcg gac agc atc agc ctc gag ctg cgc aag ccc      433
Gln Ala Asp Ser Asp Ala Asp Ser Ile Ser Leu Glu Leu Arg Lys Pro
          50          55          60

gac ggc acc ctc gtc tcc ttc acc gcc gac ttc aag aag gat gtg aag      481
Asp Gly Thr Leu Val Ser Phe Thr Ala Asp Phe Lys Lys Asp Val Lys
          65          70          75          80

gtc ttc cgg gcc ctg atc ctg ggg gag ctg gag aag ggg cag agt cag      529
Val Phe Arg Ala Leu Ile Leu Gly Glu Leu Glu Lys Gly Gln Ser Gln
          85          90          95

ttc cag gcc ctc tgc ttt gtc acc cag ctg cag cac aat gag atc atc      577
Phe Gln Ala Leu Cys Phe Val Thr Gln Leu Gln His Asn Glu Ile Ile
          100          105          110

ccc agt gag gcc atg gcc aag ctc cgg cag aaa aat ccc cgg gca gtg      625
Pro Ser Glu Ala Met Ala Lys Leu Arg Gln Lys Asn Pro Arg Ala Val
          115          120          125

cgg cag gcg gag gag gtt cgg ggt ctg gag cat ctg cac atg gat gtc      673
Arg Gln Ala Glu Glu Val Arg Gly Leu Glu His Leu His Met Asp Val
          130          135          140

gct gtc aac ttc agc cag ggg gcc ctg ctg agc ccc cat ctc cac aac      721
Ala Val Asn Phe Ser Gln Gly Ala Leu Leu Ser Pro His Leu His Asn
          145          150          155          160

gtg tgt gcc gag gcc gtg gat gcc atc tac acc cgc cag gag gat gtc      769
Val Cys Ala Glu Ala Val Asp Ala Ile Tyr Thr Arg Gln Glu Asp Val
          165          170          175

cgg ttc tgg ctg gag caa ggt gtg gac agt tct gtg ttc gag gct ctg      817
Arg Phe Trp Leu Glu Gln Gly Val Asp Ser Ser Val Phe Glu Ala Leu
          180          185          190

ccc aag gcc tca gag cag gcg gag ctg cct cgc tgc agg cag gtg ggg      865
Pro Lys Ala Ser Glu Gln Ala Glu Leu Pro Arg Cys Arg Gln Val Gly
          195          200          205

gac cac ggg aag ccc tgc gtc tgc cgc tat ggc ctg agc ctg gcc tgg      913

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Asp His Gly Lys Pro Cys Val Cys Arg Tyr Gly Leu Ser Leu Ala Trp
210                               215                               220

tac ccc tgc atg ctc aag tac tgc cac agc cgc gac cgg ccc acg ccc      961
Tyr Pro Cys Met Leu Lys Tyr Cys His Ser Arg Asp Arg Pro Thr Pro
225                               230                               235                               240

tac aag tgt ggc atc cgc agc tgc cag aag agc tac agc ttc gac ttc      1009
Tyr Lys Cys Gly Ile Arg Ser Cys Gln Lys Ser Tyr Ser Phe Asp Phe
                               245                               250                               255

tac gtg ccc cag agg cag ctg tgt ctc tgg gat gag gat ccc tac cca      1057
Tyr Val Pro Gln Arg Gln Leu Cys Leu Trp Asp Glu Asp Pro Tyr Pro
                               260                               265                               270

ggc tag ggtgggagca acctggcggg tggctgctct gggcccactg ctcttcacca      1113
Gly

gccactagag ggggtggcaa cccccacctg aggccttatt tccctccctc cccactcccc      1173

tggccctaga gcctgggccc ctctggcccc atctcacatg actgtgaagg ggggtgtggca      1233

tggcaggggg tctcatgaag gcacccccat tcccaccctg tgccttcctt gcgggcagag      1293

agggagagaa gggctcccca gatctacacc cctccctcct gcctctcccc tggagtgttc      1353

acttgcaagc tgccaaaaca tgatggcctc tggttgttct gttgaactcc ttgaacgttt      1413

agaccctaaa aggagtctat acctggacac ccacctcccc agacacaact cccttcccca      1473

tgcacacatc tggaaggagc tggcccctca gtcccttcct actccccaac aaggggctca      1533

ctatcccca aagaaggagct gttggggacc cagcagcgag cccctgtact ggattacagc      1593

atattctcat ctctggcccc gaggctgcct gtggggcgag tggagacctc ccatcactga      1653

gacagatcac agaccacgag tgcctttccc ggacctggac gttgcctcca gagcaggcac      1713

cagctctttc cctctctaca cagaaatatt tttgtaaggt tctggggcgag ggaggagca      1773

tgaagtacga ggaaaacttg aattccagat ttttagtgca aagtatttat catttctacc      1833

agaaataaac gttttaagtt tttacttgaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      1893

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      1953

aaaaa                                              1957

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<210> 17
<211> 273
<212> PRT
<213> Homo sapiens

<400> 17

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Met Arg Leu Pro Gly Val Pro Leu Ala Arg Pro Ala Leu Leu Leu Leu
1                               5                               10                               15

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Leu Pro Leu Leu Ala Pro Leu Leu Gly Thr Gly Ala Pro Ala Glu Leu
                20                               25                               30

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Arg Val Arg Val Arg Leu Pro Asp Gly Gln Val Thr Glu Glu Ser Leu
35                               40                               45

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32600PWO.ST25.txt

Gln Ala Asp Ser Asp Ala Asp Ser Ile Ser Leu Glu Leu Arg Lys Pro
50 55 60

Asp Gly Thr Leu Val Ser Phe Thr Ala Asp Phe Lys Lys Asp Val Lys
65 70 75 80

Val Phe Arg Ala Leu Ile Leu Gly Glu Leu Glu Lys Gly Gln Ser Gln
85 90 95

Phe Gln Ala Leu Cys Phe Val Thr Gln Leu Gln His Asn Glu Ile Ile
100 105 110

Pro Ser Glu Ala Met Ala Lys Leu Arg Gln Lys Asn Pro Arg Ala Val
115 120 125

Arg Gln Ala Glu Glu Val Arg Gly Leu Glu His Leu His Met Asp Val
130 135 140

Ala Val Asn Phe Ser Gln Gly Ala Leu Leu Ser Pro His Leu His Asn
145 150 155 160

Val Cys Ala Glu Ala Val Asp Ala Ile Tyr Thr Arg Gln Glu Asp Val
165 170 175

Arg Phe Trp Leu Glu Gln Gly Val Asp Ser Ser Val Phe Glu Ala Leu
180 185 190

Pro Lys Ala Ser Glu Gln Ala Glu Leu Pro Arg Cys Arg Gln Val Gly
195 200 205

Asp His Gly Lys Pro Cys Val Cys Arg Tyr Gly Leu Ser Leu Ala Trp
210 215 220

Tyr Pro Cys Met Leu Lys Tyr Cys His Ser Arg Asp Arg Pro Thr Pro
225 230 235 240

Tyr Lys Cys Gly Ile Arg Ser Cys Gln Lys Ser Tyr Ser Phe Asp Phe
245 250 255

Tyr Val Pro Gln Arg Gln Leu Cys Leu Trp Asp Glu Asp Pro Tyr Pro
260 265 270

Gly

<210> 18
<211> 2312
<212> DNA
<213> Mus musculus

<220>

<221> CDS

<222> (118)..(1857)

<223> SF03, cDNA: NM_016697, Protein: NP_057906

<400> 18

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ctgggtagcg gctcctctct tgctctgtcg ggctactgcc agacttgctg agtctcggga      60
ccgctccggc tcttattgcc actctctcgt gctctcctcg ctccccaag aagcagg      117
atg gcc ggg acc gtg cgc acc gcg tgc ttg ctg gtg gcg atg ctg cta      165
Met Ala Gly Thr Val Arg Thr Ala Cys Leu Leu Val Ala Met Leu Leu
1          5          10          15

ggc ttg ggc tgc ctg gga cag gcg cag ccc ccg ccg cct cca gac gcc      213
Gly Leu Gly Cys Leu Gly Gln Ala Gln Pro Pro Pro Pro Pro Asp Ala
20          25          30

acc tgt cac cag gtc cgt tct ttc ttc cag aga ctg cag ccc gga ctc      261
Thr Cys His Gln Val Arg Ser Phe Phe Gln Arg Leu Gln Pro Gly Leu
35          40          45

aaa tgg gtt cca gaa acc cct gta cca gga tca gat ttg caa gta tgt      309
Lys Trp Val Pro Glu Thr Pro Val Pro Gly Ser Asp Leu Gln Val Cys
50          55          60

ctc ccc aag ggc cca aca tgc tgc tca aga aag atg gaa gaa aaa tac      357
Leu Pro Lys Gly Pro Thr Cys Cys Ser Arg Lys Met Glu Glu Lys Tyr
65          70          75          80

caa cta aca gca cgg ctg aac atg gaa caa ctg ctc cag tct gcg agt      405
Gln Leu Thr Ala Arg Leu Asn Met Glu Gln Leu Leu Gln Ser Ala Ser
85          90          95

atg gaa ctc aag ttc tta att att cag aat gct gcg gtt ttc caa gag      453
Met Glu Leu Lys Phe Leu Ile Ile Gln Asn Ala Ala Val Phe Gln Glu
100          105          110

gcc ttt gaa att gtt gtt cgc cat gcc aag aac tac acc aac gcc atg      501
Ala Phe Glu Ile Val Val Arg His Ala Lys Asn Tyr Thr Asn Ala Met
115          120          125

ttc aag aat aac tac ccc agc ctg act cca caa gct ttt gag ttt gtc      549
Phe Lys Asn Asn Tyr Pro Ser Leu Thr Pro Gln Ala Phe Glu Phe Val
130          135          140

ggg gaa ttt ttc aca gat gtg tct ctc tac atc ttg ggt tct gat atc      597
Gly Glu Phe Phe Thr Asp Val Ser Leu Tyr Ile Leu Gly Ser Asp Ile
145          150          155          160

aac gtg gat gat atg gtc aat gaa ttg ttc gac agc ctc ttt cca gtc      645
Asn Val Asp Asp Met Val Asn Glu Leu Phe Asp Ser Leu Phe Pro Val
165          170          175

atc tac acc cag atg atg aac cca ggc ctg cct gag tca gtc tta gac      693
Ile Tyr Thr Gln Met Met Asn Pro Gly Leu Pro Glu Ser Val Leu Asp
180          185          190

atc aac gag tgc ctc cga gga gca aga cgt gac ctg aaa gta ttt ggc      741
Ile Asn Glu Cys Leu Arg Gly Ala Arg Arg Asp Leu Lys Val Phe Gly
195          200          205

agt ttc ccc aag ctt att atg acc cag gtt tcc aag tca ctg caa gtc      789
Ser Phe Pro Lys Leu Ile Met Thr Gln Val Ser Lys Ser Leu Gln Val
210          215          220

act cga atc ttc ctt caa gcc ctg aat ctc gga att gaa gtc atc aac      837
Thr Arg Ile Phe Leu Gln Ala Leu Asn Leu Gly Ile Glu Val Ile Asn
225          230          235          240

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32600PWO.ST25.txt

act acc gac cac ctc aag ttt agt aag gac tgt ggc cgt atg ctc acc	885
Thr Thr Asp His Leu Lys Phe Ser Lys Asp Cys Gly Arg Met Leu Thr	
245 250 255	
cga atg tgg tat tgc tct tac tgc cag gga ctg atg atg gtt aag cct	933
Arg Met Trp Tyr Cys Ser Tyr Cys Gln Gly Leu Met Met Val Lys Pro	
260 265 270	
tgc ggt ggt tat tgc aat gtg gtc atg caa ggc tgt atg gct ggt gtg	981
Cys Gly Gly Tyr Cys Asn Val Val Met Gln Gly Cys Met Ala Gly Val	
275 280 285	
gtg gag atc gac aag tac tgg aga gaa tac att ctg tct ctt gaa gag	1029
Val Glu Ile Asp Lys Tyr Trp Arg Glu Tyr Ile Leu Ser Leu Glu Glu	
290 295 300	
ctc gtg aat ggc atg tac aga atc tac gac atg gag aat gtg ctg ctc	1077
Leu Val Asn Gly Met Tyr Arg Ile Tyr Asp Met Glu Asn Val Leu Leu	
305 310 315 320	
ggc ctc ttt tct acc atc cat gat tcc atc cag tat gtg cag aag aac	1125
Gly Leu Phe Ser Thr Ile His Asp Ser Ile Gln Tyr Val Gln Lys Asn	
325 330 335	
gga ggc aag ctg acc acc acc att ggc aag ttg tgt gcc cac tcc cag	1173
Gly Gly Lys Leu Thr Thr Thr Ile Gly Lys Leu Cys Ala His Ser Gln	
340 345 350	
caa cgc caa tat aga tct gct tat tac cct gaa gat ctg ttt att gac	1221
Gln Arg Gln Tyr Arg Ser Ala Tyr Tyr Pro Glu Asp Leu Phe Ile Asp	
355 360 365	
aag aag ata tta aaa gtc gct cat gtc gaa cat gaa gaa acc tta tcc	1269
Lys Lys Ile Leu Lys Val Ala His Val Glu His Glu Glu Thr Leu Ser	
370 375 380	
agc cga aga agg gaa ctg att cag aaa ctg aag tct ttc atc aac ttc	1317
Ser Arg Arg Arg Glu Leu Ile Gln Lys Leu Lys Ser Phe Ile Asn Phe	
385 390 395 400	
tat agc gct ttg ccg ggc tac atc tgc agc cat agc ccc gtg gcc gaa	1365
Tyr Ser Ala Leu Pro Gly Tyr Ile Cys Ser His Ser Pro Val Ala Glu	
405 410 415	
aat gat acc ctg tgc tgg aac gga caa gaa ctt gtg gag aga tac agc	1413
Asn Asp Thr Leu Cys Trp Asn Gly Gln Glu Leu Val Glu Arg Tyr Ser	
420 425 430	
cag aag gcg gca agg aac ggg atg aag aat cag ttt aac ctc cat gag	1461
Gln Lys Ala Ala Arg Asn Gly Met Lys Asn Gln Phe Asn Leu His Glu	
435 440 445	
ctg aaa atg aag ggc cct gag ccg gtg gtt agc cag atc att gac aaa	1509
Leu Lys Met Lys Gly Pro Glu Pro Val Val Ser Gln Ile Ile Asp Lys	
450 455 460	
ctg aag cac att aac cag ctc ctg aga acc atg tct gtg ccc aag ggt	1557
Leu Lys His Ile Asn Gln Leu Leu Arg Thr Met Ser Val Pro Lys Gly	
465 470 475 480	
aaa gtt ctg gat aaa agc ctg gat gaa gaa gga ctt gaa agt gga gac	1605
Lys Val Leu Asp Lys Ser Leu Asp Glu Glu Gly Leu Glu Ser Gly Asp	
485 490 495	
tgc ggt gat gat gaa gat gaa tgc att gga agc tct ggt gac ggg atg	1653
Cys Gly Asp Asp Glu Asp Glu Cys Ile Gly Ser Ser Gly Asp Gly Met	
500 505 510	

32600PWO.ST25.txt

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gtg aaa gtg aag aat caa ctg cgc ttc ctt gca gaa ctg gcc tat gat      1701
Val Lys Val Lys Asn Gln Leu Arg Phe Leu Ala Glu Leu Ala Tyr Asp
      515                      520                      525

ctg gat gtg gac gat gct ccg ggg aac aag cag cat gga aat cag aag      1749
Leu Asp Val Asp Asp Ala Pro Gly Asn Lys Gln His Gly Asn Gln Lys
      530                      535                      540

gac aac gag atc acc acc tct cac agc gtg ggg aac atg ccg tcc cca      1797
Asp Asn Glu Ile Thr Thr Ser His Ser Val Gly Asn Met Pro Ser Pro
      545                      550                      555                      560

ctg aag atc ctc atc agt gtg gcc atc tat gtg gcg tgc ttt ttt ttc      1845
Leu Lys Ile Leu Ile Ser Val Ala Ile Tyr Val Ala Cys Phe Phe Phe
      565                      570                      575

ctg gtg cac tga cttgccagcg tccagtgcct gtgctgccct gcagcacctg      1897
Leu Val His

tggtccctac agaaaggag ccaccttctt ttttttttct tttttttttt ttttttatct      1957

tttatgcctc ctcccaccac cattaagtag gagactaacc gcgtgttatg ttttcgaaaa      2017

tcaaattggta tctttatgag gatggtaaat tttagtggta ggatagattg tctttttgca      2077

aagaaaaaaaa aaaccttcaa gttgtgccaa attattttct tacatttgac tgttggaaca      2137

tggttgtcat gtttccctct tttctctttc tctgcatgga tttctttgac aaaaaaaaaa      2197

taaataaaca ttcaaataaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      2257

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa      2312

<210> 19
<211> 579
<212> PRT
<213> Mus musculus

<400> 19

Met Ala Gly Thr Val Arg Thr Ala Cys Leu Leu Val Ala Met Leu Leu
1                      5                      10                      15

Gly Leu Gly Cys Leu Gly Gln Ala Gln Pro Pro Pro Pro Pro Asp Ala
20                      25                      30

Thr Cys His Gln Val Arg Ser Phe Phe Gln Arg Leu Gln Pro Gly Leu
35                      40                      45

Lys Trp Val Pro Glu Thr Pro Val Pro Gly Ser Asp Leu Gln Val Cys
50                      55                      60

Leu Pro Lys Gly Pro Thr Cys Cys Ser Arg Lys Met Glu Glu Lys Tyr
65                      70                      75                      80

Gln Leu Thr Ala Arg Leu Asn Met Glu Gln Leu Leu Gln Ser Ala Ser
85                      90                      95

Met Glu Leu Lys Phe Leu Ile Ile Gln Asn Ala Ala Val Phe Gln Glu

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100

105

110

Ala Phe Glu Ile Val Val Arg His Ala Lys Asn Tyr Thr Asn Ala Met
 115 120 125

Phe Lys Asn Asn Tyr Pro Ser Leu Thr Pro Gln Ala Phe Glu Phe Val
 130 135 140

Gly Glu Phe Phe Thr Asp Val Ser Leu Tyr Ile Leu Gly Ser Asp Ile
 145 150 155 160

Asn Val Asp Asp Met Val Asn Glu Leu Phe Asp Ser Leu Phe Pro Val
 165 170 175

Ile Tyr Thr Gln Met Met Asn Pro Gly Leu Pro Glu Ser Val Leu Asp
 180 185 190

Ile Asn Glu Cys Leu Arg Gly Ala Arg Arg Asp Leu Lys Val Phe Gly
 195 200 205

Ser Phe Pro Lys Leu Ile Met Thr Gln Val Ser Lys Ser Leu Gln Val
 210 215 220

Thr Arg Ile Phe Leu Gln Ala Leu Asn Leu Gly Ile Glu Val Ile Asn
 225 230 235 240

Thr Thr Asp His Leu Lys Phe Ser Lys Asp Cys Gly Arg Met Leu Thr
 245 250 255

Arg Met Trp Tyr Cys Ser Tyr Cys Gln Gly Leu Met Met Val Lys Pro
 260 265 270

Cys Gly Gly Tyr Cys Asn Val Val Met Gln Gly Cys Met Ala Gly Val
 275 280 285

Val Glu Ile Asp Lys Tyr Trp Arg Glu Tyr Ile Leu Ser Leu Glu Glu
 290 295 300

Leu Val Asn Gly Met Tyr Arg Ile Tyr Asp Met Glu Asn Val Leu Leu
 305 310 315 320

Gly Leu Phe Ser Thr Ile His Asp Ser Ile Gln Tyr Val Gln Lys Asn
 325 330 335

Gly Gly Lys Leu Thr Thr Thr Ile Gly Lys Leu Cys Ala His Ser Gln
 340 345 350

Gln Arg Gln Tyr Arg Ser Ala Tyr Tyr Pro Glu Asp Leu Phe Ile Asp
 355 360 365

Lys Lys Ile Leu Lys Val Ala His Val Glu His Glu Glu Thr Leu Ser

370

375

380

Ser Arg Arg Arg Glu Leu Ile Gln Lys Leu Lys Ser Phe Ile Asn Phe
 385 390 395 400

Tyr Ser Ala Leu Pro Gly Tyr Ile Cys Ser His Ser Pro Val Ala Glu
 405 410 415

Asn Asp Thr Leu Cys Trp Asn Gly Gln Glu Leu Val Glu Arg Tyr Ser
 420 425 430

Gln Lys Ala Ala Arg Asn Gly Met Lys Asn Gln Phe Asn Leu His Glu
 435 440 445

Leu Lys Met Lys Gly Pro Glu Pro Val Val Ser Gln Ile Ile Asp Lys
 450 455 460

Leu Lys His Ile Asn Gln Leu Leu Arg Thr Met Ser Val Pro Lys Gly
 465 470 475 480

Lys Val Leu Asp Lys Ser Leu Asp Glu Glu Gly Leu Glu Ser Gly Asp
 485 490 495

Cys Gly Asp Asp Glu Asp Glu Cys Ile Gly Ser Ser Gly Asp Gly Met
 500 505 510

Val Lys Val Lys Asn Gln Leu Arg Phe Leu Ala Glu Leu Ala Tyr Asp
 515 520 525

Leu Asp Val Asp Asp Ala Pro Gly Asn Lys Gln His Gly Asn Gln Lys
 530 535 540

Asp Asn Glu Ile Thr Thr Ser His Ser Val Gly Asn Met Pro Ser Pro
 545 550 555 560

Leu Lys Ile Leu Ile Ser Val Ala Ile Tyr Val Ala Cys Phe Phe Phe
 565 570 575

Leu Val His

<210> 20
 <211> 2382
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (191)..(1933)
 <223> SF03, cDNA: NM_004484, Protein: NP_004475

<400> 20
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60

32600PWO.ST25.txt

aactttttgca gcggtctgggt agcagcacgt ctcttgcctc tcagggccac tgccaggctt	120
gccgagtcct gggactgctc tcgctccggc tgccactctc ccgcgctctc ctagctccct	180
gcgaagcagg atg gcc ggg acc gtg cgc acc gcg tgc ttg gtg gtg gcg Met Ala Gly Thr Val Arg Thr Ala Cys Leu Val Val Ala 1 5 10	229
atg ctg ctc agc ttg gac ttc ccg gga cag gcg cag ccc ccg ccg ccg Met Leu Leu Ser Leu Asp Phe Pro Gly Gln Ala Gln Pro Pro Pro Pro 15 20 25	277
ccg ccg gac gcc acc tgt cac caa gtc cgc tcc ttc ttc cag aga ctg Pro Pro Asp Ala Thr Cys His Gln Val Arg Ser Phe Phe Gln Arg Leu 30 35 40 45	325
cag ccc gga ctc aag tgg gtg cca gaa act ccc gtg cca gga tca gat Gln Pro Gly Leu Lys Trp Val Pro Glu Thr Pro Val Pro Gly Ser Asp 50 55 60	373
ttg caa gta tgt ctc cct aag ggc cca aca tgc tgc tca aga aag atg Leu Gln Val Cys Leu Pro Lys Gly Pro Thr Cys Cys Ser Arg Lys Met 65 70 75	421
gaa gaa aaa tac caa cta aca gca cga ttg aac atg gaa cag ctg ctt Glu Glu Lys Tyr Gln Leu Thr Ala Arg Leu Asn Met Glu Gln Leu Leu 80 85 90	469
cag tct gca agt atg gag ctc aag ttc tta att att cag aat gct gcg Gln Ser Ala Ser Met Glu Lys Phe Leu Ile Ile Gln Asn Ala Ala 95 100 105	517
gtt ttc caa gag gcc ttt gaa att gtt gtt cgc cat gcc aag aac tac Val Phe Gln Glu Ala Phe Glu Ile Val Val Arg His Ala Lys Asn Tyr 110 115 120 125	565
acc aat gcc atg ttc aag aac aac tac cca agc ctg act cca caa gct Thr Asn Ala Met Phe Lys Asn Asn Tyr Pro Ser Leu Thr Pro Gln Ala 130 135 140	613
ttt gag ttt gtg ggt gaa ttt ttc aca gat gtg tct ctc tac atc ttg Phe Glu Phe Val Gly Glu Phe Phe Thr Asp Val Ser Leu Tyr Ile Leu 145 150 155	661
ggt tct gac atc aat gta gat gac atg gtc aat gaa ttg ttt gac agc Gly Ser Asp Ile Asn Val Asp Asp Met Val Asn Glu Leu Phe Asp Ser 160 165 170	709
ctg ttt cca gtc atc tat acc cag cta atg aac cca ggc ctg cct gat Leu Phe Pro Val Ile Tyr Thr Gln Leu Met Asn Pro Gly Leu Pro Asp 175 180 185	757
tca gcc ttg gac atc aat gag tgc ctc cga gga gca aga cgt gac ctg Ser Ala Leu Asp Ile Asn Glu Cys Leu Arg Gly Ala Arg Arg Asp Leu 190 195 200 205	805
aaa gta ttt ggg aat ttc ccc aag ctt att atg acc cag gtt tcc aag Lys Val Phe Gly Asn Phe Pro Lys Leu Ile Met Thr Gln Val Ser Lys 210 215 220	853
tca ctg caa gtc act agg atc ttc ctt cag gct ctg aat ctt gga att Ser Leu Gln Val Thr Arg Ile Phe Leu Gln Ala Leu Asn Leu Gly Ile 225 230 235	901
gaa gtg atc aac aca act gat cac ctg aag ttc agt aag gac tgt ggc Glu Val Ile Asn Thr Thr Asp His Leu Lys Phe Ser Lys Asp Cys Gly 240 245 250	949

32600PWO.ST25.txt

cga atg ctc acc aga atg tgg tac tgc tct tac tgc cag gga ctg atg Arg Met Leu Thr Arg Met Trp Tyr Cys Ser Tyr Cys Gln Gly Leu Met 255 260 265	997
atg gtt aaa ccc tgt ggc ggt tac tgc aat gtg gtc atg caa ggc tgt Met Val Lys Pro Cys Gly Gly Tyr Cys Asn Val Val Met Gln Gly Cys 270 275 280 285	1045
atg gca ggt gtg gtg gag att gac aag tac tgg aga gaa tac att ctg Met Ala Gly Val Val Glu Ile Asp Lys Tyr Trp Arg Glu Tyr Ile Leu 290 295 300	1093
tcc ctt gaa gaa ctt gtg aat ggc atg tac aga atc tat gac atg gag Ser Leu Glu Glu Leu Val Asn Gly Met Tyr Arg Ile Tyr Asp Met Glu 305 310 315	1141
aac gta ctg ctt ggt ctc ttt tca aca atc cat gat tct atc cag tat Asn Val Leu Leu Gly Leu Phe Ser Thr Ile His Asp Ser Ile Gln Tyr 320 325 330	1189
gtc cag aag aat gca gga aag ctg acc acc act att ggc aag tta tgt Val Gln Lys Asn Ala Gly Lys Leu Thr Thr Thr Ile Gly Lys Leu Cys 335 340 345	1237
gcc cat tct caa caa cgc caa tat aga tct gct tat tat cct gaa gat Ala His Ser Gln Gln Arg Gln Tyr Arg Ser Ala Tyr Tyr Pro Glu Asp 350 355 360 365	1285
ctc ttt att gac aag aaa gta tta aaa gtt gct cat gta gaa cat gaa Leu Phe Ile Asp Lys Lys Val Leu Lys Val Ala His Val Glu His Glu 370 375 380	1333
gaa acc tta tcc agc cga aga agg gaa cta att cag aag ttg aag tct Glu Thr Leu Ser Ser Arg Arg Arg Glu Leu Ile Gln Lys Leu Lys Ser 385 390 395	1381
ttc atc agc ttc tat agt gct ttg cct ggc tac atc tgc agc cat agc Phe Ile Ser Phe Tyr Ser Ala Leu Pro Gly Tyr Ile Cys Ser His Ser 400 405 410	1429
cct gtg gcg gaa aac gac acc ctt tgc tgg aat gga caa gaa ctc gtg Pro Val Ala Glu Asn Asp Thr Leu Cys Trp Asn Gly Gln Glu Leu Val 415 420 425	1477
gag aga tac agc caa aag gca gca agg aat gga atg aaa aac cag ttc Glu Arg Tyr Ser Gln Lys Ala Ala Arg Asn Gly Met Lys Asn Gln Phe 430 435 440 445	1525
aat ctc cat gag ctg aaa atg aag ggc cct gag cca gtg gtc agt caa Asn Leu His Glu Leu Lys Met Lys Gly Pro Glu Pro Val Val Ser Gln 450 455 460	1573
att att gac aaa ctg aag cac att aac cag ctc ctg aga acc atg tct Ile Ile Asp Lys Leu Lys His Ile Asn Gln Leu Leu Arg Thr Met Ser 465 470 475	1621
atg ccc aaa ggt aga gtt ctg gat aaa aac ctg gat gag gaa ggg ttt Met Pro Lys Gly Arg Val Leu Asp Lys Asn Leu Asp Glu Glu Gly Phe 480 485 490	1669
gaa agt gga gac tgc ggt gat gat gaa gat gag tgc att gga ggc tct Glu Ser Gly Asp Cys Gly Asp Asp Glu Asp Glu Cys Ile Gly Gly Ser 495 500 505	1717
ggt gat gga atg ata aaa gtg aag aat cag ctc cgc ttc ctt gca gaa Gly Asp Gly Met Ile Lys Val Lys Asn Gln Leu Arg Phe Leu Ala Glu 510 515 520 525	1765

32600PWO.ST25.txt

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ctg gcc tat gat ctg gat gtg gat gat gcg cct gga aac agt cag cag      1813
Leu Ala Tyr Asp Leu Asp Val Asp Asp Ala Pro Gly Asn Ser Gln Gln
                    530                    535                    540

gca act ccg aag gac aac gag ata agc acc ttt cac aac ctc ggg aac      1861
Ala Thr Pro Lys Asp Asn Glu Ile Ser Thr Phe His Asn Leu Gly Asn
                    545                    550                    555

gtt cat tcc ccg ctg aag ctt ctc acc agc atg gcc atc tcg gtg gtg      1909
Val His Ser Pro Leu Lys Leu Leu Thr Ser Met Ala Ile Ser Val Val
                    560                    565                    570

tgc ttc ttc ttc ctg gtg cac tga ctgcctgggtg cccagcacat gtgctgccct      1963
Cys Phe Phe Phe Leu Val His
                    575                    580

acagcaccct gtgggtcttcc tcgataaagg gaaccacttt cttattttttt tctattttttt      2023

tttttttggt atcctgtata cctcctccag ccatgaagta gaggactaac catgtgttat      2083

gttttcgaaa atcaaattggt atcttttgga ggaagataca ttttagtggt agcatataga      2143

ttgtcctttt gcaaagaaag aaaaaaaaaacc atcaagttgt gccaaattat tctcctatgt      2203

ttggctgcta gaacatgggt accatgtctt tctctctcac tccctccctt tctatcgttc      2263

tctctttgca tggattttctt tgaaaaaaaa taaattgctc aaataaaaaa aaaaaaaaaa      2323

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      2382

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<210> 21
<211> 580
<212> PRT
<213> Homo sapiens

<400> 21

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Met Ala Gly Thr Val Arg Thr Ala Cys Leu Val Val Ala Met Leu Leu
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Ser Leu Asp Phe Pro Gly Gln Ala Gln Pro Pro Pro Pro Pro Pro Asp
20                    25                    30

Ala Thr Cys His Gln Val Arg Ser Phe Phe Gln Arg Leu Gln Pro Gly
35                    40                    45

Leu Lys Trp Val Pro Glu Thr Pro Val Pro Gly Ser Asp Leu Gln Val
50                    55                    60

Cys Leu Pro Lys Gly Pro Thr Cys Cys Ser Arg Lys Met Glu Glu Lys
65                    70                    75                    80

Tyr Gln Leu Thr Ala Arg Leu Asn Met Glu Gln Leu Leu Gln Ser Ala
85                    90                    95

Ser Met Glu Leu Lys Phe Leu Ile Ile Gln Asn Ala Ala Val Phe Gln
100                   105                   110

Glu Ala Phe Glu Ile Val Val Arg His Ala Lys Asn Tyr Thr Asn Ala
22

```

115

120

125

Met Phe Lys Asn Asn Tyr Pro Ser Leu Thr Pro Gln Ala Phe Glu Phe
 130 135 140

Val Gly Glu Phe Phe Thr Asp Val Ser Leu Tyr Ile Leu Gly Ser Asp
 145 150 155 160

Ile Asn Val Asp Asp Met Val Asn Glu Leu Phe Asp Ser Leu Phe Pro
 165 170 175

Val Ile Tyr Thr Gln Leu Met Asn Pro Gly Leu Pro Asp Ser Ala Leu
 180 185 190

Asp Ile Asn Glu Cys Leu Arg Gly Ala Arg Arg Asp Leu Lys Val Phe
 195 200 205

Gly Asn Phe Pro Lys Leu Ile Met Thr Gln Val Ser Lys Ser Leu Gln
 210 215 220

Val Thr Arg Ile Phe Leu Gln Ala Leu Asn Leu Gly Ile Glu Val Ile
 225 230 235 240

Asn Thr Thr Asp His Leu Lys Phe Ser Lys Asp Cys Gly Arg Met Leu
 245 250 255

Thr Arg Met Trp Tyr Cys Ser Tyr Cys Gln Gly Leu Met Met Val Lys
 260 265 270

Pro Cys Gly Gly Tyr Cys Asn Val Val Met Gln Gly Cys Met Ala Gly
 275 280 285

Val Val Glu Ile Asp Lys Tyr Trp Arg Glu Tyr Ile Leu Ser Leu Glu
 290 295 300

Glu Leu Val Asn Gly Met Tyr Arg Ile Tyr Asp Met Glu Asn Val Leu
 305 310 315 320

Leu Gly Leu Phe Ser Thr Ile His Asp Ser Ile Gln Tyr Val Gln Lys
 325 330 335

Asn Ala Gly Lys Leu Thr Thr Thr Ile Gly Lys Leu Cys Ala His Ser
 340 345 350

Gln Gln Arg Gln Tyr Arg Ser Ala Tyr Tyr Pro Glu Asp Leu Phe Ile
 355 360 365

Asp Lys Lys Val Leu Lys Val Ala His Val Glu His Glu Glu Thr Leu
 370 375 380

Ser Ser Arg Arg Arg Glu Leu Ile Gln Lys Leu Lys Ser Phe Ile Ser

385 390 395 400

Phe Tyr Ser Ala Leu Pro Gly Tyr Ile Cys Ser His Ser Pro Val Ala
405 410 415

Glu Asn Asp Thr Leu Cys Trp Asn Gly Gln Glu Leu Val Glu Arg Tyr
420 425 430

Ser Gln Lys Ala Ala Arg Asn Gly Met Lys Asn Gln Phe Asn Leu His
435 440 445

Glu Leu Lys Met Lys Gly Pro Glu Pro Val Val Ser Gln Ile Ile Asp
450 455 460

Lys Leu Lys His Ile Asn Gln Leu Leu Arg Thr Met Ser Met Pro Lys
465 470 475 480

Gly Arg Val Leu Asp Lys Asn Leu Asp Glu Glu Gly Phe Glu Ser Gly
485 490 495

Asp Cys Gly Asp Asp Glu Asp Glu Cys Ile Gly Gly Ser Gly Asp Gly
500 505 510

Met Ile Lys Val Lys Asn Gln Leu Arg Phe Leu Ala Glu Leu Ala Tyr
515 520 525

Asp Leu Asp Val Asp Asp Ala Pro Gly Asn Ser Gln Gln Ala Thr Pro
530 535 540

Lys Asp Asn Glu Ile Ser Thr Phe His Asn Leu Gly Asn Val His Ser
545 550 555 560

Pro Leu Lys Leu Leu Thr Ser Met Ala Ile Ser Val Val Cys Phe Phe
565 570 575

Phe Leu Val His
580

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<212> DNA
<213> Mus musculus
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<222> (89)..(1138)
<223> SF04, cDNA: NM_007443, Protein: NP_031469
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gacatcaaag accaaagacc acagagcc atg cag ggt ctc agg acc ctg ttc 112
                        Met Gln Gly Leu Arg Thr Leu Phe
                        1           5

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32600PWO.ST25.txt

ctg ctg ctg act gcc tgc ctc gct tcg agg gct gac cct gcg tca aca	160
Leu Leu Leu Thr Ala Cys Leu Ala Ser Arg Ala Asp Pro Ala Ser Thr	
10 15 20	
ctg cca gat atc cag gtt cag gag aac ttc agt gag tcc cgg atc tat	208
Leu Pro Asp Ile Gln Val Gln Glu Asn Phe Ser Glu Ser Arg Ile Tyr	
25 30 35 40	
gga aaa tgg tac aac ctg gcg gtg gga tcc acc tgc ccg tgg ctg agc	256
Gly Lys Trp Tyr Asn Leu Ala Val Gly Ser Thr Cys Pro Trp Leu Ser	
45 50 55	
cgc att aag gac aag atg agc gtg agc acg ctg gtg ctg cag gag ggg	304
Arg Ile Lys Asp Lys Met Ser Val Ser Thr Leu Val Leu Gln Glu Gly	
60 65 70	
gcg aca gaa aca gag atc agc atg acc agt act cga tgg cgg aga ggt	352
Ala Thr Glu Thr Glu Ile Ser Met Thr Ser Thr Arg Trp Arg Arg Gly	
75 80 85	
gtc tgt gag gag atc act ggg gcg tac cag aag acg gac atc gat gga	400
Val Cys Glu Glu Ile Thr Gly Ala Tyr Gln Lys Thr Asp Ile Asp Gly	
90 95 100	
aag ttc ctc tac cac aaa tcc aaa tgg aac ata acc ttg gaa tcc tat	448
Lys Phe Leu Tyr His Lys Ser Lys Trp Asn Ile Thr Leu Glu Ser Tyr	
105 110 115 120	
gtg gtc cac acc aac tat gac gaa tat gcc att ttc ctt acc aag aag	496
Val Val His Thr Asn Tyr Asp Glu Tyr Ala Ile Phe Leu Thr Lys Lys	
125 130 135	
tcc agc cac cac cac ggg ctc acc atc act gcc aag ctc tat ggt cgg	544
Ser Ser His His His Gly Leu Thr Ile Thr Ala Lys Leu Tyr Gly Arg	
140 145 150	
gag cca cag ctg agg gac agc ctt ctg cag gag ttc aag gat gtg gcc	592
Glu Pro Gln Leu Arg Asp Ser Leu Leu Gln Glu Phe Lys Asp Val Ala	
155 160 165	
ctg aat gtg ggc atc tct gag aac tcc atc att ttt atg cct gac aga	640
Leu Asn Val Gly Ile Ser Glu Asn Ser Ile Ile Phe Met Pro Asp Arg	
170 175 180	
ggg gaa tgt gtc cct ggg gat cgg gag gtg gag ccc aca tca att gcc	688
Gly Glu Cys Val Pro Gly Asp Arg Glu Val Glu Pro Thr Ser Ile Ala	
185 190 195 200	
aga gcc cgg cgg gca gtg ctg ccc caa gag agt gag ggg tca ggg act	736
Arg Ala Arg Arg Ala Val Leu Pro Gln Glu Ser Glu Gly Ser Gly Thr	
205 210 215	
gag cca cta ata act ggg acc ctc aag aaa gaa gac tcc tgc cag ctc	784
Glu Pro Leu Ile Thr Gly Thr Leu Lys Lys Glu Asp Ser Cys Gln Leu	
220 225 230	
aat tac tca gaa ggc ccc tgc cta ggg atg caa gag agg tat tac tac	832
Asn Tyr Ser Glu Gly Pro Cys Leu Gly Met Gln Glu Arg Tyr Tyr Tyr	
235 240 245	
aac ggc gct tcc atg gcc tgc gag acc ttt caa tat ggg ggt tgc cta	880
Asn Gly Ala Ser Met Ala Cys Glu Thr Phe Gln Tyr Gly Gly Cys Leu	
250 255 260	
ggc aac ggc aac aac ttc atc tct gag aag gac tgt ctg cag aca tgt	928
Gly Asn Gly Asn Asn Phe Ile Ser Glu Lys Asp Cys Leu Gln Thr Cys	
265 270 275 280	

32600PWO.ST25.txt

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cgg acc ata gcg gcc tgc aat ctc ccc ata gtc caa ggc ccc tgc cga      976
Arg Thr Ile Ala Ala Cys Asn Leu Pro Ile Val Gln Gly Pro Cys Arg
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gcc ttc ata aag ctc tgg gca ttt gat gca gca caa ggg aag tgc atc      1024
Ala Phe Ile Lys Leu Trp Ala Phe Asp Ala Ala Gln Gly Lys Cys Ile
                300                305                310

caa ttc cac tac ggg ggc tgc aaa ggc aac ggc aac aaa ttc tac tct      1072
Gln Phe His Tyr Gly Gly Cys Lys Gly Asn Gly Asn Lys Phe Tyr Ser
                315                320                325

gag aag gaa tgc aaa gag tac tgt gga gtc cct ggt gat ggg tac gag      1120
Glu Lys Glu Cys Lys Glu Tyr Cys Gly Val Pro Gly Asp Gly Tyr Glu
                330                335                340

gaa cta ata cgc agt tga aggtgccagt ctgcaagcca gagggtagcc      1168
Glu Leu Ile Arg Ser
345

actgtttgtc acagcgcagt ccagcttaga tgatctggac ccaaataaaaa caagttgtca      1228

cttcct      1234

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<212> PRT
<213> Mus musculus

<400> 23

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Asn Phe Ser Glu Ser Arg Ile Tyr Gly Lys Trp Tyr Asn Leu Ala Val
                35                40                45

Gly Ser Thr Cys Pro Trp Leu Ser Arg Ile Lys Asp Lys Met Ser Val
50                55                60

Ser Thr Leu Val Leu Gln Glu Gly Ala Thr Glu Thr Glu Ile Ser Met
65                70                75                80

Thr Ser Thr Arg Trp Arg Arg Gly Val Cys Glu Glu Ile Thr Gly Ala
                85                90                95

Tyr Gln Lys Thr Asp Ile Asp Gly Lys Phe Leu Tyr His Lys Ser Lys
100                105                110

Trp Asn Ile Thr Leu Glu Ser Tyr Val Val His Thr Asn Tyr Asp Glu
115                120                125

Tyr Ala Ile Phe Leu Thr Lys Lys Ser Ser His His His Gly Leu Thr
130                135                140

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32600PWO.ST25.txt

Ile Thr Ala Lys Leu Tyr Gly Arg Glu Pro Gln Leu Arg Asp Ser Leu
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Leu Gln Glu Phe Lys Asp Val Ala Leu Asn Val Gly Ile Ser Glu Asn
165 170 175

Ser Ile Ile Phe Met Pro Asp Arg Gly Glu Cys Val Pro Gly Asp Arg
180 185 190

Glu Val Glu Pro Thr Ser Ile Ala Arg Ala Arg Arg Ala Val Leu Pro
195 200 205

Gln Glu Ser Glu Gly Ser Gly Thr Glu Pro Leu Ile Thr Gly Thr Leu
210 215 220

Lys Lys Glu Asp Ser Cys Gln Leu Asn Tyr Ser Glu Gly Pro Cys Leu
225 230 235 240

Gly Met Gln Glu Arg Tyr Tyr Tyr Asn Gly Ala Ser Met Ala Cys Glu
245 250 255

Thr Phe Gln Tyr Gly Gly Cys Leu Gly Asn Gly Asn Asn Phe Ile Ser
260 265 270

Glu Lys Asp Cys Leu Gln Thr Cys Arg Thr Ile Ala Ala Cys Asn Leu
275 280 285

Pro Ile Val Gln Gly Pro Cys Arg Ala Phe Ile Lys Leu Trp Ala Phe
290 295 300

Asp Ala Ala Gln Gly Lys Cys Ile Gln Phe His Tyr Gly Gly Cys Lys
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Gly Asn Gly Asn Lys Phe Tyr Ser Glu Lys Glu Cys Lys Glu Tyr Cys
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Gly Val Pro Gly Asp Gly Tyr Glu Glu Leu Ile Arg Ser
340 345

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<211> 1413
<212> DNA
<213> Homo sapiens

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<222> (227)..(1285)
<223> SF04, cDNA: NM_001633, Protein: NP_001624

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gggctgtaat tggccccagc tgagcagggc aaacactgag gtcaactaca agccacaggc 120

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cccttcccca gcctcagttc acagctgccc tgttgcaggg aggcggtggc ccttctgttg      180
ctagaccgag cctgtgggat ataccaaggc agaggagccc atagcc atg agg agc      235
                               Met Arg Ser
                               1

ctc ggg gcc ctg ctc ttg ctg ctg agc gcc tgc ctg gcg gtg agc gct      283
Leu Gly Ala Leu Leu Leu Leu Leu Ser Ala Cys Leu Ala Val Ser Ala
    5                10                15

ggc cct gtg cca acg ccg ccc gac aac atc caa gtg cag gaa aac ttc      331
Gly Pro Val Pro Thr Pro Pro Asp Asn Ile Gln Val Gln Glu Asn Phe
20                25                30                35

aat atc tct cgg atc tat ggg aag tgg tac aac ctg gcc atc ggt tcc      379
Asn Ile Ser Arg Ile Tyr Gly Lys Trp Tyr Asn Leu Ala Ile Gly Ser
    40                45                50

acc tgc ccc tgg ctg aag aag atc atg gac agg atg aca gtg agc acg      427
Thr Cys Pro Trp Leu Lys Lys Ile Met Asp Arg Met Thr Val Ser Thr
    55                60                65

ctg gtg ctg gga gag ggc gct aca gag gcg gag atc agc atg acc agc      475
Leu Val Leu Gly Glu Gly Ala Thr Glu Ala Glu Ile Ser Met Thr Ser
    70                75                80

act cgt tgg cgg aaa ggt gtc tgt gag gag acg tct gga gct tat gag      523
Thr Arg Trp Arg Lys Gly Val Cys Glu Glu Thr Ser Gly Ala Tyr Glu
    85                90                95

aaa aca gat act gat ggg aag ttt ctc tat cac aaa tcc aaa tgg aac      571
Lys Thr Asp Thr Asp Gly Lys Phe Leu Tyr His Lys Ser Lys Trp Asn
100                105                110                115

ata acc atg gag tcc tat gtg gtc cac acc aac tat gat gag tat gcc      619
Ile Thr Met Glu Ser Tyr Val Val His Thr Asn Tyr Asp Glu Tyr Ala
    120                125                130

att ttc ctg acc aag aaa ttc agc cgc cat cat gga ccc acc att act      667
Ile Phe Leu Thr Lys Lys Phe Ser Arg His His Gly Pro Thr Ile Thr
    135                140                145

gcc aag ctc tac ggg cgg gcg ccg cag ctg agg gaa act ctc ctg cag      715
Ala Lys Leu Tyr Gly Arg Ala Pro Gln Leu Arg Glu Thr Leu Leu Gln
    150                155                160

gac ttc aga gtg gtt gcc cag ggt gtg ggc atc cct gag gac tcc atc      763
Asp Phe Arg Val Val Ala Gln Gly Val Gly Ile Pro Glu Asp Ser Ile
    165                170                175

ttc acc atg gct gac cga ggt gaa tgt gtc cct ggg gag cag gaa cca      811
Phe Thr Met Ala Asp Arg Gly Glu Cys Val Pro Gly Glu Gln Glu Pro
180                185                190                195

gag ccc atc tta atc ccg aga gtc cgg agg gct gtg cta ccc caa gaa      859
Glu Pro Ile Leu Ile Pro Arg Val Arg Arg Ala Val Leu Pro Gln Glu
    200                205                210

gag gaa gga tca ggg ggt ggg caa ctg gta act gaa gtc acc aag aaa      907
Glu Glu Gly Ser Gly Gly Gly Gln Leu Val Thr Glu Val Thr Lys Lys
    215                220                225

gaa gat tcc tgc cag ctg ggc tac tgc gcc ggt ccc tgc atg gga atg      955
Glu Asp Ser Cys Gln Leu Gly Tyr Ser Ala Gly Pro Cys Met Gly Met
    230                235                240

acc agc agg tat ttc tat aat ggt aca tcc atg gcc tgt gag act ttc      1003

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32600PWO.ST25.txt

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Gln	Tyr	Gly	Gly	Cys	Met	Gly	Asn	Gly	Asn	Asn	Phe	Val	Thr	Glu	Lys		
260					265				270						275		
gag	tgt	ctg	cag	acc	tgc	cga	act	gtg	gcg	gcc	tgc	aat	ctc	ccc	ata	1099	
Glu	Cys	Leu	Gln	Thr	Cys	Arg	Thr	Val	Ala	Ala	Cys	Asn	Leu	Pro	Ile		
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gtc	cgg	ggc	ccc	tgc	cga	gcc	ttc	atc	cag	ctc	tgg	gca	ttt	gat	gct	1147	
Val	Arg	Gly	Pro	Cys	Arg	Ala	Phe	Ile	Gln	Leu	Trp	Ala	Phe	Asp	Ala		
			295					300					305				
gtc	aag	ggg	aag	tgc	gtc	ctc	ttc	ccc	tac	ggg	ggc	tgc	cag	ggc	aac	1195	
Val	Lys	Gly	Lys	Cys	Val	Leu	Phe	Pro	Tyr	Gly	Gly	Cys	Gln	Gly	Asn		
		310					315					320					
ggg	aac	aag	ttc	tac	tca	gag	aag	gag	tgc	aga	gag	tac	tgc	ggg	gtc	1243	
Gly	Asn	Lys	Phe	Tyr	Ser	Glu	Lys	Glu	Cys	Arg	Glu	Tyr	Cys	Gly	Val		
		325				330					335						
cct	ggg	gat	ggg	gat	gag	gag	ctg	ctg	cgc	ttc	tcc	aac	tga			1285	
Pro	Gly	Asp	Gly	Asp	Glu	Glu	Leu	Leu	Arg	Phe	Ser	Asn					
340					345					350							
caactggccg	gtctgcaagt	cagaggatgg	ccagtgtctg	tcccgggggtc	ctgtggcagg											1345	
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 <211> 352
 <212> PRT
 <213> Homo sapiens

<400> 25

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			20					25					30			
Glu	Asn	Phe	Asn	Ile	Ser	Arg	Ile	Tyr	Gly	Lys	Trp	Tyr	Asn	Leu	Ala	
		35					40					45				
Ile	Gly	Ser	Thr	Cys	Pro	Trp	Leu	Lys	Lys	Ile	Met	Asp	Arg	Met	Thr	
	50					55					60					
Val	Ser	Thr	Leu	Val	Leu	Gly	Glu	Gly	Ala	Thr	Glu	Ala	Glu	Ile	Ser	
65					70					75					80	
Met	Thr	Ser	Thr	Arg	Trp	Arg	Lys	Gly	Val	Cys	Glu	Glu	Thr	Ser	Gly	
				85					90					95		
Ala	Tyr	Glu	Lys	Thr	Asp	Thr	Asp	Gly	Lys	Phe	Leu	Tyr	His	Lys	Ser	
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32600PWO.ST25.txt

Lys Trp Asn Ile Thr Met Glu Ser Tyr Val Val His Thr Asn Tyr Asp
 115 120 125

Glu Tyr Ala Ile Phe Leu Thr Lys Lys Phe Ser Arg His His Gly Pro
 130 135 140

Thr Ile Thr Ala Lys Leu Tyr Gly Arg Ala Pro Gln Leu Arg Glu Thr
 145 150 155 160

Leu Leu Gln Asp Phe Arg Val Val Ala Gln Gly Val Gly Ile Pro Glu
 165 170 175

Asp Ser Ile Phe Thr Met Ala Asp Arg Gly Glu Cys Val Pro Gly Glu
 180 185 190

Gln Glu Pro Glu Pro Ile Leu Ile Pro Arg Val Arg Arg Ala Val Leu
 195 200 205

Pro Gln Glu Glu Glu Gly Ser Gly Gly Gly Gln Leu Val Thr Glu Val
 210 215 220

Thr Lys Lys Glu Asp Ser Cys Gln Leu Gly Tyr Ser Ala Gly Pro Cys
 225 230 235 240

Met Gly Met Thr Ser Arg Tyr Phe Tyr Asn Gly Thr Ser Met Ala Cys
 245 250 255

Glu Thr Phe Gln Tyr Gly Gly Cys Met Gly Asn Gly Asn Asn Phe Val
 260 265 270

Thr Glu Lys Glu Cys Leu Gln Thr Cys Arg Thr Val Ala Ala Cys Asn
 275 280 285

Leu Pro Ile Val Arg Gly Pro Cys Arg Ala Phe Ile Gln Leu Trp Ala
 290 295 300

Phe Asp Ala Val Lys Gly Lys Cys Val Leu Phe Pro Tyr Gly Gly Cys
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32600PWO.ST25.txt

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<223> SF05, cDNA: NM_009250, Protein: NP_033276

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 Met Thr Tyr Leu Glu Leu
 1 5

ctt gct ttg ctg gcc ttg caa agt gtg gtg aca ggg gca acg ttc cca 163
 Leu Ala Leu Leu Ala Leu Gln Ser Val Val Thr Gly Ala Thr Phe Pro
 10 15 20

gat gaa acc ata act gag tgg tca gtg aac atg tat aac cac ctt cga 211
 Asp Glu Thr Ile Thr Glu Trp Ser Val Asn Met Tyr Asn His Leu Arg
 25 30 35

ggc acc ggg gaa gat gaa aac att ctc ttc tct cca cta agc att gcc 259
 Gly Thr Gly Glu Asp Glu Asn Ile Leu Phe Ser Pro Leu Ser Ile Ala
 40 45 50

ctt gcg atg gga atg atg gag ctt ggg gct caa gga tct act agg aaa 307
 Leu Ala Met Gly Met Met Glu Leu Gly Ala Gln Gly Ser Thr Arg Lys
 55 60 65 70

gaa atc cgc cat tca atg gga tat gag ggt ctg aaa ggt ggt gaa gaa 355
 Glu Ile Arg His Ser Met Gly Tyr Glu Gly Leu Lys Gly Gly Glu Glu
 75 80 85

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 Phe Ser Phe Leu Arg Asp Phe Ser Asn Met Ala Ser Ala Glu Glu Asn
 90 95 100

caa tat gtg atg aaa ctt gcc aat tgc ctc ttt gta caa aat gga ttt 451
 Gln Tyr Val Met Lys Leu Ala Asn Ser Leu Phe Val Gln Asn Gly Phe
 105 110 115

cat gtc aat gag gaa ttc ttg caa atg ctg aaa atg tac ttt aat gca 499
 His Val Asn Glu Glu Phe Leu Gln Met Leu Lys Met Tyr Phe Asn Ala
 120 125 130

gaa gtc aac cat gtg gac ttc agt caa aat gtg gct gtg gct aac tcc 547
 Glu Val Asn His Val Asp Phe Ser Gln Asn Val Ala Val Ala Asn Ser
 135 140 145 150

atc aat aaa tgg gtg gag aat tat aca aac agt ctg ttg aaa gat ctg 595
 Ile Asn Lys Trp Val Glu Asn Tyr Thr Asn Ser Leu Leu Lys Asp Leu
 155 160 165

gtg tct ccg gag gac ttt gat ggt gtc act aat ttg gcc ctc atc aat 643
 Val Ser Pro Glu Asp Phe Asp Gly Val Thr Asn Leu Ala Leu Ile Asn
 170 175 180

gct gta tat ttc aaa gga aac tgg aag tct cag ttt aga cct gaa aat 691
 Ala Val Tyr Phe Lys Gly Asn Trp Lys Ser Gln Phe Arg Pro Glu Asn
 185 190 195

acc aga act ttc tcc ttc acg aaa gat gat gaa agt gaa gtg cag att 739
 Thr Arg Thr Phe Ser Phe Thr Lys Asp Asp Glu Ser Glu Val Gln Ile
 200 205 210

cca atg atg tat caa caa gga gaa ttt tat tat ggt gaa ttt agt gat 787
 Pro Met Met Tyr Gln Gln Gly Glu Phe Tyr Tyr Gly Glu Phe Ser Asp
 215 220 225 230

gga tcc aat gag gct ggt ggt atc tac caa gtc ctt gag ata ccc tat 835

32600PWO.ST25.txt

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Glu	Gly	Asp	Glu	Ile	Ser	Met	Met	Leu	Ala	Leu	Ser	Arg	Gln	Glu	Val		
			250					255					260				
cca	ctg	gcc	aca	ctg	gag	cct	ctg	ctc	aaa	gca	cag	ctg	atc	gaa	gaa		931
Pro	Leu	Ala	Thr	Leu	Glu	Pro	Leu	Leu	Lys	Ala	Gln	Leu	Ile	Glu	Glu		
		265					270					275					
tgg	gca	aac	tct	gtg	aag	aaa	caa	aag	gtg	gaa	gtg	tac	ttg	ccc	agg		979
Trp	Ala	Asn	Ser	Val	Lys	Lys	Gln	Lys	Val	Glu	Val	Tyr	Leu	Pro	Arg		
	280					285					290						
ttc	act	gtg	gaa	cag	gaa	att	gat	tta	aaa	gac	atc	ttg	aaa	gcc	ctt		1027
Phe	Thr	Val	Glu	Gln	Glu	Ile	Asp	Leu	Lys	Asp	Ile	Leu	Lys	Ala	Leu		
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Gly	Val	Thr	Glu	Ile	Phe	Ile	Lys	Asp	Ala	Asn	Leu	Thr	Ala	Met	Ser		
				315					320					325			
gat	aag	aaa	gag	ctg	ttc	ctc	tcc	aaa	gct	gtt	cac	aag	tcc	tgc	att		1123
Asp	Lys	Lys	Glu	Leu	Phe	Leu	Ser	Lys	Ala	Val	His	Lys	Ser	Cys	Ile		
			330					335					340				
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Glu	Val	Asn	Glu	Glu	Gly	Ser	Glu	Ala	Ala	Ala	Ala	Ser	Gly	Met	Ile		
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Pro	Phe	Leu	Tyr	Leu	Ile	Arg	Asn	Arg	Lys	Ser	Gly	Ile	Ile	Leu	Phe		
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Phe	Glu	Glu	Leu														
			410														
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taggaggaaa	tgtgggatat	gtaagacca	tagatgtata	ttttgtatat	ctgtagtatt												1910
atacttttaa	tttattaaag	tataactctt	ttattttattt	ttaaaagt	cctgtgaacc												1970
aatatgccac	atgactctac	tagcaagttc	agatatctca	ttagctattc	tggaatgacat												2030

32600PWO.ST25.txt

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caagaggcct catggagga atcccggtgta ccatttacgt tttagtgtgatt ttttgtgtgatg 2090
ttcacacaaa gatgaaatca cattgttgca cactctctag actatatcca agaaagggcat 2150
caagtgggtac attggtgtgc caggaaaata gatgtaatta ctttattaaa aaagttcctg 2210
gtattgtgca tcatatggaa tcagtgtgtc ttaaacttag tacgtcctgc tgacacctgg 2270
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aaaaaaaaaa aaaa 2944

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<210> 27
<211> 410
<212> PRT
<213> Mus musculus

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<400> 27

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1          5          10          15

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Thr Gly Ala Thr Phe Pro Asp Glu Thr Ile Thr Glu Trp Ser Val Asn
          20          25          30

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```

Met Tyr Asn His Leu Arg Gly Thr Gly Glu Asp Glu Asn Ile Leu Phe
          35          40          45

```

```

Ser Pro Leu Ser Ile Ala Leu Ala Met Gly Met Met Glu Leu Gly Ala
          50          55          60

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```

Gln Gly Ser Thr Arg Lys Glu Ile Arg His Ser Met Gly Tyr Glu Gly
65          70          75          80

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```

Leu Lys Gly Gly Glu Glu Phe Ser Phe Leu Arg Asp Phe Ser Asn Met
          85          90          95

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Ala Ser Ala Glu Glu Asn Gln Tyr Val Met Lys Leu Ala Asn Ser Leu
          100          105          110

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32600PWO.ST25.txt

Phe Val Gln Asn Gly Phe His Val Asn Glu Glu Phe Leu Gln Met Leu
 115 120 125
 Lys Met Tyr Phe Asn Ala Glu Val Asn His Val Asp Phe Ser Gln Asn
 130 135 140
 Val Ala Val Ala Asn Ser Ile Asn Lys Trp Val Glu Asn Tyr Thr Asn
 145 150 155 160
 Ser Leu Leu Lys Asp Leu Val Ser Pro Glu Asp Phe Asp Gly Val Thr
 165 170 175
 Asn Leu Ala Leu Ile Asn Ala Val Tyr Phe Lys Gly Asn Trp Lys Ser
 180 185 190
 Gln Phe Arg Pro Glu Asn Thr Arg Thr Phe Ser Phe Thr Lys Asp Asp
 195 200 205
 Glu Ser Glu Val Gln Ile Pro Met Met Tyr Gln Gln Gly Glu Phe Tyr
 210 215 220
 Tyr Gly Glu Phe Ser Asp Gly Ser Asn Glu Ala Gly Gly Ile Tyr Gln
 225 230 235 240
 Val Leu Glu Ile Pro Tyr Glu Gly Asp Glu Ile Ser Met Met Leu Ala
 245 250 255
 Leu Ser Arg Gln Glu Val Pro Leu Ala Thr Leu Glu Pro Leu Leu Lys
 260 265 270
 Ala Gln Leu Ile Glu Glu Trp Ala Asn Ser Val Lys Lys Gln Lys Val
 275 280 285
 Glu Val Tyr Leu Pro Arg Phe Thr Val Glu Gln Glu Ile Asp Leu Lys
 290 295 300
 Asp Ile Leu Lys Ala Leu Gly Val Thr Glu Ile Phe Ile Lys Asp Ala
 305 310 315 320
 Asn Leu Thr Ala Met Ser Asp Lys Lys Glu Leu Phe Leu Ser Lys Ala
 325 330 335
 Val His Lys Ser Cys Ile Glu Val Asn Glu Glu Gly Ser Glu Ala Ala
 340 345 350
 Ala Ala Ser Gly Met Ile Ala Ile Ser Arg Met Ala Val Leu Tyr Pro
 355 360 365
 Gln Val Ile Val Asp His Pro Phe Leu Tyr Leu Ile Arg Asn Arg Lys
 370 375 380

32600PWO.ST25.txt

Ser Gly Ile Ile Leu Phe Met Gly Arg Val Met Asn Pro Glu Thr Met
 385 390 395 400

Asn Thr Ser Gly His Asp Phe Glu Glu Leu
 405 410

<210> 28
 <211> 1910
 <212> DNA
 <213> Homo sapiens

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 <223> SF05, cDNA: NM_005025, Protein: NP_005016

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 cgcgttgggt taggaaaccg gtgcaaaacc tctcgggtga aagatttaca tttttcgact 240
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 ttggtttgag ttgcaccagt aaaactgttc tgggagatct gaagattgag aaaaatcctg 360
 ctaattgagg acgaggtgga tggtatctgg tggatgttat aggcttgaaa ctgttacaat 420
 atg gct ttc ctt gga ctc ttc tct ttg ctg gtt ctg caa agt atg gct 468
 Met Ala Phe Leu Gly Leu Phe Ser Leu Leu Val Leu Gln Ser Met Ala
 1 5 10 15
 aca ggg gcc act ttc cct gag gaa gcc att gct gac ttg tca gtg aat 516
 Thr Gly Ala Thr Phe Pro Glu Glu Ala Ile Ala Asp Leu Ser Val Asn
 20 25 30
 atg tac aat cgt ctt aga gcc act ggt gaa gat gaa aat att ctc ttc 564
 Met Tyr Asn Arg Leu Arg Ala Thr Gly Glu Asp Glu Asn Ile Leu Phe
 35 40 45
 tct cca ttg agt att gct ctt gca atg gga atg atg gaa ctt ggg gcc 612
 Ser Pro Leu Ser Ile Ala Leu Ala Met Gly Met Met Glu Leu Gly Ala
 50 55 60
 caa gga tct acc cag aaa gaa atc cgc cac tca atg gga tat gac agc 660
 Gln Gly Ser Thr Gln Lys Glu Ile Arg His Ser Met Gly Tyr Asp Ser
 65 70 75 80
 cta aaa aat ggt gaa gaa ttt tct ttc ttg aag gag ttt tca aac atg 708
 Leu Lys Asn Gly Glu Glu Phe Ser Phe Leu Lys Glu Phe Ser Asn Met
 85 90 95
 gta act gct aaa gag agc caa tat gtg atg aaa att gcc aat tcc ttg 756
 Val Thr Ala Lys Glu Ser Gln Tyr Val Met Lys Ile Ala Asn Ser Leu
 100 105 110
 ttt gtg caa aat gga ttt cat gtc aat gag gag ttt ttg caa atg atg 804
 Phe Val Gln Asn Gly Phe His Val Asn Glu Glu Phe Leu Gln Met Met
 115 120 125
 aaa aaa tat ttt aat gca gca gta aat cat gtg gac ttc agt caa aat 852
 35

32600PWO.ST25.txt

Lys	Lys	Tyr	Phe	Asn	Ala	Ala	Val	Asn	His	Val	Asp	Phe	Ser	Gln	Asn	
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Val	Ala	Val	Ala	Asn	Tyr	Ile	Asn	Lys	Trp	Val	Glu	Asn	Asn	Thr	Asn	
145				150					155						160	
aat	ctg	gtg	aaa	gat	ttg	gta	tcc	cca	agg	gat	ttt	gat	gct	gcc	act	948
Asn	Leu	Val	Lys	Asp	Leu	Val	Ser	Pro	Arg	Asp	Phe	Asp	Ala	Ala	Thr	
				165					170					175		
tat	ctg	gcc	ctc	att	aat	gct	gtc	tat	ttc	aag	ggg	aac	tgg	aag	tcg	996
Tyr	Leu	Ala	Leu	Ile	Asn	Ala	Val	Tyr	Phe	Lys	Gly	Asn	Trp	Lys	Ser	
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cag	ttt	agg	cct	gaa	aat	act	aga	acc	ttt	tct	ttc	act	aaa	gat	gat	1044
Gln	Phe	Arg	Pro	Glu	Asn	Thr	Arg	Thr	Phe	Ser	Phe	Thr	Lys	Asp	Asp	
		195					200					205				
gaa	agt	gaa	gtc	caa	att	cca	atg	atg	tat	cag	caa	gga	gaa	ttt	tat	1092
Glu	Ser	Glu	Val	Gln	Ile	Pro	Met	Met	Tyr	Gln	Gln	Gly	Glu	Phe	Tyr	
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tat	ggg	gaa	ttt	agt	gat	ggc	tcc	aat	gaa	gct	ggg	ggg	atc	tac	caa	1140
Tyr	Gly	Glu	Phe	Ser	Asp	Gly	Ser	Asn	Glu	Ala	Gly	Gly	Ile	Tyr	Gln	
225					230					235					240	
gtc	cta	gaa	ata	cca	tat	gaa	gga	gat	gaa	ata	agc	atg	atg	ctg	gtg	1188
Val	Leu	Glu	Ile	Pro	Tyr	Glu	Gly	Asp	Glu	Ile	Ser	Met	Met	Leu	Val	
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ctg	tcc	aga	cag	gaa	gtt	cct	ctt	gct	act	ctg	gag	cca	tta	gtc	aaa	1236
Leu	Ser	Arg	Gln	Glu	Val	Pro	Leu	Ala	Thr	Leu	Glu	Pro	Leu	Val	Lys	
			260					265					270			
gca	cag	ctg	gtt	gaa	gaa	tgg	gca	aac	tct	gtg	aag	aag	caa	aaa	gta	1284
Ala	Gln	Leu	Val	Glu	Glu	Trp	Ala	Asn	Ser	Val	Lys	Lys	Gln	Lys	Val	
		275					280					285				
gaa	gta	tac	ctg	ccc	agg	ttc	aca	gtg	gaa	cag	gaa	att	gat	tta	aaa	1332
Glu	Val	Tyr	Leu	Pro	Arg	Phe	Thr	Val	Glu	Gln		Ile	Asp	Leu	Lys	
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gat	gtt	ttg	aag	gct	ctt	gga	ata	act	gaa	att	ttc	atc	aaa	gat	gca	1380
Asp	Val	Leu	Lys	Ala	Leu	Gly	Ile	Thr	Glu	Ile	Phe	Ile	Lys	Asp	Ala	
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Asn	Leu	Thr	Gly	Leu	Ser	Asp	Asn	Lys	Glu	Ile	Phe	Leu	Ser	Lys	Ala	
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att	cac	aag	tcc	ttc	cta	gag	gtt	aat	gaa	gaa	ggc	tca	gaa	gct	gct	1476
Ile	His	Lys	Ser	Phe	Leu	Glu	Val	Asn	Glu	Glu	Gly	Ser	Glu	Ala	Ala	
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gct	gtc	tca	gga	atg	att	gca	att	agt	agg	atg	gct	gtg	ctg	tat	cct	1524
Ala	Val	Ser	Gly	Met	Ile	Ala	Ile	Ser	Arg	Met	Ala	Val	Leu	Tyr	Pro	
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caa	gtt	att	gtc	gac	cat	cca	ttt	ttc	ttt	ctt	atc	aga	aac	agg	aga	1572
Gln	Val	Ile	Val	Asp	His	Pro	Phe	Phe	Phe	Leu	Ile	Arg	Asn	Arg	Arg	
	370					375					380					
act	ggg	aca	att	cta	ttc	atg	gga	cga	gtc	atg	cat	cct	gaa	aca	atg	1620
Thr	Gly	Thr	Ile	Leu	Phe	Met	Gly	Arg	Val	Met	His	Pro	Glu	Thr	Met	
385					390					395					400	
aac	aca	agt	gga	cat	gat	ttc	gaa	gaa	ctt	taa	gttacttttat	ttgaataaca				1673

32600PWO.ST25.txt

Asn Thr Ser Gly His Asp Phe Glu Glu Leu
 405 410

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 ataagtaact tgtcaaggaa tggtatcagt attaagctaa tggtcctgtt atgtcattgt 1853
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 <212> PRT
 <213> Homo sapiens

<400> 29

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 20 25 30

Met Tyr Asn Arg Leu Arg Ala Thr Gly Glu Asp Glu Asn Ile Leu Phe
 35 40 45

Ser Pro Leu Ser Ile Ala Leu Ala Met Gly Met Met Glu Leu Gly Ala
 50 55 60

Gln Gly Ser Thr Gln Lys Glu Ile Arg His Ser Met Gly Tyr Asp Ser
 65 70 75 80

Leu Lys Asn Gly Glu Glu Phe Ser Phe Leu Lys Glu Phe Ser Asn Met
 85 90 95

Val Thr Ala Lys Glu Ser Gln Tyr Val Met Lys Ile Ala Asn Ser Leu
 100 105 110

Phe Val Gln Asn Gly Phe His Val Asn Glu Glu Phe Leu Gln Met Met
 115 120 125

Lys Lys Tyr Phe Asn Ala Ala Val Asn His Val Asp Phe Ser Gln Asn
 130 135 140

Val Ala Val Ala Asn Tyr Ile Asn Lys Trp Val Glu Asn Asn Thr Asn
 145 150 155 160

Asn Leu Val Lys Asp Leu Val Ser Pro Arg Asp Phe Asp Ala Ala Thr
 165 170 175

Tyr Leu Ala Leu Ile Asn Ala Val Tyr Phe Lys Gly Asn Trp Lys Ser
 180 185 190

Gln Phe Arg Pro Glu Asn Thr Arg Thr Phe Ser Phe Thr Lys Asp Asp

195

200

205

Glu Ser Glu Val Gln Ile Pro Met Met Tyr Gln Gln Gly Glu Phe Tyr
 210 215 220

Tyr Gly Glu Phe Ser Asp Gly Ser Asn Glu Ala Gly Gly Ile Tyr Gln
 225 230 235 240

Val Leu Glu Ile Pro Tyr Glu Gly Asp Glu Ile Ser Met Met Leu Val
 245 250 255

Leu Ser Arg Gln Glu Val Pro Leu Ala Thr Leu Glu Pro Leu Val Lys
 260 265 270

Ala Gln Leu Val Glu Glu Trp Ala Asn Ser Val Lys Lys Gln Lys Val
 275 280 285

Glu Val Tyr Leu Pro Arg Phe Thr Val Glu Gln Glu Ile Asp Leu Lys
 290 295 300

Asp Val Leu Lys Ala Leu Gly Ile Thr Glu Ile Phe Ile Lys Asp Ala
 305 310 315 320

Asn Leu Thr Gly Leu Ser Asp Asn Lys Glu Ile Phe Leu Ser Lys Ala
 325 330 335

Ile His Lys Ser Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala
 340 345 350

Ala Val Ser Gly Met Ile Ala Ile Ser Arg Met Ala Val Leu Tyr Pro
 355 360 365

Gln Val Ile Val Asp His Pro Phe Phe Phe Leu Ile Arg Asn Arg Arg
 370 375 380

Thr Gly Thr Ile Leu Phe Met Gly Arg Val Met His Pro Glu Thr Met
 385 390 395 400

Asn Thr Ser Gly His Asp Phe Glu Glu Leu
 405 410

<210> 30
 <211> 2202
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (23)..(697)
 <223> SF06, cDNA: NM_172633, Protein: NP_766221

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52

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gac ttt ggc tcc agc ctg ggg gcg gtg ctg gcc ctg ctg ttg ctg ctg Asp Phe Gly Ser Ser Leu Gly Ala Val Leu Ala Leu Leu Leu Leu Leu 30 35 40	148
ctg ccc gcc tgc tgc ccc gta agg gct cag aac gac acg gag ccc atc Leu Pro Ala Cys Cys Pro Val Arg Ala Gln Asn Asp Thr Glu Pro Ile 45 50 55	196
gtg cta gag ggc aag tgc ctg gta gtg tgc gat tcc agc cca tcg ggg Val Leu Glu Gly Lys Cys Leu Val Val Cys Asp Ser Ser Pro Ser Gly 60 65 70	244
gat ggc gcc gtc act tct tcc ctg ggc att tct gtg cgc tca ggc agt Asp Gly Ala Val Thr Ser Ser Leu Gly Ile Ser Val Arg Ser Gly Ser 75 80 85 90	292
gcc aag gtg gcc ttc tcc gct act cgg agc acc aac cac gag ccg tca Ala Lys Val Ala Phe Ser Ala Thr Arg Ser Thr Asn His Glu Pro Ser 95 100 105	340
gag atg agc aac cgt acc atg acc atc tac ttc gac cag gtc tta gta Glu Met Ser Asn Arg Thr Met Thr Ile Tyr Phe Asp Gln Val Leu Val 110 115 120	388
aac att ggc aac cac ttt gac ctt gcc tcc agt ata ttt gta gca cca Asn Ile Gly Asn His Phe Asp Leu Ala Ser Ser Ile Phe Val Ala Pro 125 130 135	436
aga aag gga att tat agc ttc agc ttc cac gtg gtc aaa gtg tac aac Arg Lys Gly Ile Tyr Ser Phe Ser Phe His Val Val Lys Val Tyr Asn 140 145 150	484
aga caa act atc cag gtc agc tta atg cag aat ggc tac ccg gtg atc Arg Gln Thr Ile Gln Val Ser Leu Met Gln Asn Gly Tyr Pro Val Ile 155 160 165 170	532
tct gca ttt gcc gga gac cag gat gtt acc agg gaa gca gcc agc aat Ser Ala Phe Ala Gly Asp Gln Asp Val Thr Arg Glu Ala Ala Ser Asn 175 180 185	580
ggc gtt ctg ctg ctc atg gaa aga gaa gac aaa gtt cat ctc aaa cta Gly Val Leu Leu Leu Met Glu Arg Glu Asp Lys Val His Leu Lys Leu 190 195 200	628
gag aga ggc aac ctc atg gga ggc tgg aaa tac tcc aca ttc tcg ggc Glu Arg Gly Asn Leu Met Gly Gly Trp Lys Tyr Ser Thr Phe Ser Gly 205 210 215	676
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32600PWO.ST25.txt

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<212> PRT
<213> Mus musculus

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<400> 31

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Gly Arg Arg Gly Ala Leu Arg Glu Pro Ala Asp Phe Gly Ser Ser Leu
          20           25           30

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Gly Ala Val Leu Ala Leu Leu Leu Leu Leu Pro Ala Cys Cys Pro
          35           40           45

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Val Arg Ala Gln Asn Asp Thr Glu Pro Ile Val Leu Glu Gly Lys Cys
          50           55           60

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Leu Val Val Cys Asp Ser Ser Pro Ser Gly Asp Gly Ala Val Thr Ser
65           70           75           80

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32600PWO.ST25.txt

Ser Leu Gly Ile Ser Val Arg Ser Gly Ser Ala Lys Val Ala Phe Ser
85 90 95

Ala Thr Arg Ser Thr Asn His Glu Pro Ser Glu Met Ser Asn Arg Thr
100 105 110

Met Thr Ile Tyr Phe Asp Gln Val Leu Val Asn Ile Gly Asn His Phe
115 120 125

Asp Leu Ala Ser Ser Ile Phe Val Ala Pro Arg Lys Gly Ile Tyr Ser
130 135 140

Phe Ser Phe His Val Val Lys Val Tyr Asn Arg Gln Thr Ile Gln Val
145 150 155 160

Ser Leu Met Gln Asn Gly Tyr Pro Val Ile Ser Ala Phe Ala Gly Asp
165 170 175

Gln Asp Val Thr Arg Glu Ala Ala Ser Asn Gly Val Leu Leu Leu Met
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Glu Arg Glu Asp Lys Val His Leu Lys Leu Glu Arg Gly Asn Leu Met
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Gly Gly Trp Lys Tyr Ser Thr Phe Ser Gly Phe Leu Val Phe Pro Leu
210 215 220

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<211> 2750
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (564)..(1238)
<223> SF06, cDNA: NM_182511, Protein: NP_872317

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cgcgccgcct cccaccagtc ccg atg cag gcg ccc ggc cgg ggg cca ctc ggg 593

32600PWO.ST25.txt
Met Gln Ala Pro Gly Arg Gly Pro Leu Gly
1 5 10

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ctg ccc gcc tgc tgc ccc gtg cgg gcg cag aac gac acg gag ccc atc Leu Pro Ala Cys Cys Pro Val Arg Ala Gln Asn Asp Thr Glu Pro Ile 45 50 55	737
gtg ctg gag ggc aag tgc ctg gtg gtg tgc gac tcc agc ccg tcg gcg Val Leu Glu Gly Lys Cys Leu Val Val Cys Asp Ser Ser Pro Ser Ala 60 65 70	785
gac ggc gcc gtc acc tcc tcc cta ggc atc tcc gtg cgc tcc ggc agc Asp Gly Ala Val Thr Ser Ser Leu Gly Ile Ser Val Arg Ser Gly Ser 75 80 85 90	833
gcc aag gtg gcc ttc tcc gcc acg cgg agc acc aac cac gag ccg tcc Ala Lys Val Ala Phe Ser Ala Thr Arg Ser Thr Asn His Glu Pro Ser 95 100 105	881
gag atg agc aac cgc acc atg acc atc tat ttc gac cag gta tta gta Glu Met Ser Asn Arg Thr Met Thr Ile Tyr Phe Asp Gln Val Leu Val 110 115 120	929
aat att ggc aac cac ttt gat ctt gct tcc agt ata ttt gta gca ccg Asn Ile Gly Asn His Phe Asp Leu Ala Ser Ser Ile Phe Val Ala Pro 125 130 135	977
aga aaa ggg att tat agc ttc agc ttc cac gtg gtc aaa gtg tat aac Arg Lys Gly Ile Tyr Ser Phe Ser Phe His Val Val Lys Val Tyr Asn 140 145 150	1025
aga caa acc atc cag gtc agt tta atg cag aat ggc tac cca gtg atc Arg Gln Thr Ile Gln Val Ser Leu Met Gln Asn Gly Tyr Pro Val Ile 155 160 165 170	1073
tcg gcc ttt gca gga gac cag gat gtc acc aga gaa gct gct agc aat Ser Ala Phe Ala Gly Asp Gln Asp Val Thr Arg Glu Ala Ala Ser Asn 175 180 185	1121
ggc gtg ctg ctg ctc atg gaa agg gaa gac aaa gtg cat ctc aaa ctt Gly Val Leu Leu Leu Met Glu Arg Glu Asp Lys Val His Leu Lys Leu 190 195 200	1169
gag aga ggc aac ctc atg ggg ggc tgg aaa tac tcc aca ttc tcg ggc Glu Arg Gly Asn Leu Met Gly Gly Trp Lys Tyr Ser Thr Phe Ser Gly 205 210 215	1217
ttc ttg gtg ttt cct cta taa acacagagcc ccctagatgg tgggggaatg Phe Leu Val Phe Pro Leu 220	1268
gcaaactgga cccaggactc cgccctttaa aacaccctga acttactgga attggacacc	1328
ttgtttccaa cctccgtcag actgttgacag tagaagaatg atttcctttg aaacctccag	1388
tacttttggtt ttgttttttt ggaatactga caattcctcg ggaacctggc ctctaattag	1448
ttttagatga caaggtctta aggagaaatg aaattatcga tttgagcaat ttgtacctgt	1508
gattgtaaag tcaatatcgg attttattgt tgggaccatg gacctctttt gtttgtatgt	1568

32600PWO.ST25.txt

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tgtattgtcg tcccaacgga aggagagctc ctgactccag gatgggctgc aggttgcagt 1628
cagggcctga agtaggagcc cagcaaagaa ccacctgctg gacagtcctt gacatgtgtt 1688
ctgtgtgtgt ctgtatagcc ttaagaaaaa gaatggcttc actttcattc tgtattcttc 1748
ccccaccat gtggctggga ggacttgga gggggatggg gacattggga acctgtcaag 1808
aagtgcctta tccagagaag caaatTTTgc acgattggac tgcaattttt gttttgtatt 1868
gtttgtgttt tttcttgaaa agctttactt ttctttccac actcagctct cctcctcaa 1928
ccccactttt atttttcttg ctgggggtga ggagagaaaa tatagaattc ctggataaga 1988
ccaaacaaaa caaacatta aaatacctgt atgttttgtt ttagacgaga ccaaactaaa 2048
caaaaagtat ctgtttatca aagtaaaagt aacacaatgg acaattctgc ttattctctc 2108
aaagagattc taagatgcac ctttagaact attaatagca acctgcattt ttttttaatt 2168
tatacttcag aatcctttaa gaacctggtg ttcctgagtg gtcctgaatc atataagttg 2228
gtaatggaag ctgtaatgac caagtcccct aaacatacta tgtctttgcc acgtgtgctg 2288
tgacttctct gtgggtgatt taatttatTT ggatccacct ctgagtgagc gcacagtgat 2348
caggtgcttc aaagccaaca gaccagctcc tcttctccg gatcctcttt tgatctgccc 2408
aggaaagggg tgcattgaca ctctcctgca tgcacctggc gagaagccac ctgaaagtca 2468
ctgtgggttaa agatattggt ggaggtaccc caggagcact gttacaaatc cttcttgttt 2528
tggtcatctc tacaacatta ttaagacaca gctgagagtt gatgggtgtg taatgcatat 2588
gccaaaggaaa tgtcactaat ccaaagcaa tcaaaaagga gacctcaaac cagatgttaa 2648
tttgttcttt gtgtaacaat gtaacaaaaa tattgatgat aaaagtcata atttaagatt 2708
cagaataaat ggggttgatg tctggcaaaa aaaaaaaaaa aa 2750

```

```

<210> 33
<211> 224
<212> PRT
<213> Homo sapiens

```

```
<400> 33
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Met Gln Ala Pro Gly Arg Gly Pro Leu Gly Leu Arg Leu Met Met Pro
1          5          10          15
```

```
Gly Arg Arg Gly Ala Leu Arg Glu Pro Gly Gly Cys Gly Ser Cys Leu
          20          25          30
```

```
Gly Val Ala Leu Ala Leu Leu Leu Leu Leu Pro Ala Cys Cys Pro
          35          40          45
```

```
Val Arg Ala Gln Asn Asp Thr Glu Pro Ile Val Leu Glu Gly Lys Cys
          50          55          60
```

```
Leu Val Val Cys Asp Ser Ser Pro Ser Ala Asp Gly Ala Val Thr Ser
65          70          75          80
```

32600PWO.ST25.txt

Ser Leu Gly Ile Ser Val Arg Ser Gly Ser Ala Lys Val Ala Phe Ser
85 90 95

Ala Thr Arg Ser Thr Asn His Glu Pro Ser Glu Met Ser Asn Arg Thr
100 105 110

Met Thr Ile Tyr Phe Asp Gln Val Leu Val Asn Ile Gly Asn His Phe
115 120 125

Asp Leu Ala Ser Ser Ile Phe Val Ala Pro Arg Lys Gly Ile Tyr Ser
130 135 140

Phe Ser Phe His Val Val Lys Val Tyr Asn Arg Gln Thr Ile Gln Val
145 150 155 160

Ser Leu Met Gln Asn Gly Tyr Pro Val Ile Ser Ala Phe Ala Gly Asp
165 170 175

Gln Asp Val Thr Arg Glu Ala Ala Ser Asn Gly Val Leu Leu Leu Met
180 185 190

Glu Arg Glu Asp Lys Val His Leu Lys Leu Glu Arg Gly Asn Leu Met
195 200 205

Gly Gly Trp Lys Tyr Ser Thr Phe Ser Gly Phe Leu Val Phe Pro Leu
210 215 220

<210> 34
<211> 1542
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (131)..(1258)
<223> SF07, cDNA: NM_026840, Protein: NP_081116

<400> 34
cccagtgaaa ccgaatcctc cagctctggt gtcccaggcg ccgcctcccc tctgcgcccc 60
tgccctgccc tggacagcct gtcgcgccgt ctgcagtcct gaactattct gcaggtcacc 120
agccctgaag atg aag ttt tgg ctg ctg ctc gga ctt ctg ttg cta cac 169
Met Lys Phe Trp Leu Leu Leu Gly Leu Leu Leu Leu His
1 5 10
gaa gcg ctg gaa gat gtt gct ggc cag cat tct cct aag aac aag cgt 217
Glu Ala Leu Glu Asp Val Ala Gly Gln His Ser Pro Lys Asn Lys Arg
15 20 25
cca aag gag caa gga gaa aac aga atc aaa cca acc aac aaa aag gcc 265
Pro Lys Glu Gln Gly Glu Asn Arg Ile Lys Pro Thr Asn Lys Lys Ala
30 35 40 45
aaa ccc aag att cct aag gta aag gac agg gac tcc act gac tca acc 313
Lys Pro Lys Ile Pro Lys Val Lys Asp Arg Asp Ser Thr Asp Ser Thr
50 55 60

32600PWO.ST25.txt

gca aag agc cag tcc atc atg atg caa gcg atg ggc aac ggt cgc ttc Ala Lys Ser Gln Ser Ile Met Met Gln Ala Met Gly Asn Gly Arg Phe 65 70 75	361
cag agg cct gct gcc aca gtg agt ctc ctg gca ggg caa act cta gag Gln Arg Pro Ala Ala Thr Val Ser Leu Leu Ala Gly Gln Thr Leu Glu 80 85 90	409
cta cga tgt aag gga agc aaa gtg gag tgg agt tac ccc gcc tac ttg Leu Arg Cys Lys Gly Ser Lys Val Glu Trp Ser Tyr Pro Ala Tyr Leu 95 100 105	457
gac acc ttc aag gac tcc cgc ctc act gtg aag cag agt gaa cgc tat Asp Thr Phe Lys Asp Ser Arg Leu Thr Val Lys Gln Ser Glu Arg Tyr 110 115 120 125	505
ggg cag ttg act ctg gtc aac tcc acc gcg gcc gac acc ggt gaa ttc Gly Gln Leu Thr Leu Val Asn Ser Thr Ala Ala Asp Thr Gly Glu Phe 130 135 140	553
agc tgc tgg gag caa ctg tgc aat ggc tac atc tgc aga cgg gat gaa Ser Cys Trp Glu Gln Leu Cys Asn Gly Tyr Ile Cys Arg Arg Asp Glu 145 150 155	601
gcc aaa aca ggc tcc acc tat atc ttc ttc aca gag aaa gga gag ctg Ala Lys Thr Gly Ser Thr Tyr Ile Phe Phe Thr Glu Lys Gly Glu Leu 160 165 170	649
ttt gtg cct tct ccc agt tac ttt gat gtt gtc tac ctg aac ccg gac Phe Val Pro Ser Pro Ser Tyr Phe Asp Val Val Tyr Leu Asn Pro Asp 175 180 185	697
aga caa gct gtg gtt cct tgt cga gtg aca gcc cca tca gcc aaa gtc Arg Gln Ala Val Val Pro Cys Arg Val Thr Ala Pro Ser Ala Lys Val 190 195 200 205	745
acg ctc cac agg gag ttt ccc gcc aaa gaa atc cct gcc aat ggc acg Thr Leu His Arg Glu Phe Pro Ala Lys Glu Ile Pro Ala Asn Gly Thr 210 215 220	793
gac att gtg tac gac atg aag aga ggt ttc gtg tac ctt cag cct cat Asp Ile Val Tyr Asp Met Lys Arg Gly Phe Val Tyr Leu Gln Pro His 225 230 235	841
tcc gat cac cag ggt gtg gtc tac tgc aaa gcg gaa gcc ggg ggc aag Ser Asp His Gln Gly Val Val Tyr Cys Lys Ala Glu Ala Gly Gly Lys 240 245 250	889
tct cag atc tca gtc aag tat cag ctg ctc tat gta gag gtt cct agt Ser Gln Ile Ser Val Lys Tyr Gln Leu Leu Tyr Val Glu Val Pro Ser 255 260 265	937
ggc cct cca tca aca acc atc ttg gcc tcc tct aac aaa gtg agg ggc Gly Pro Pro Ser Thr Thr Ile Leu Ala Ser Ser Asn Lys Val Arg Gly 270 275 280 285	985
ggt gat gac atc agc gtg ctc tgc act gtc ctc ggg gag cct gat gtg Gly Asp Asp Ile Ser Val Leu Cys Thr Val Leu Gly Glu Pro Asp Val 290 295 300	1033
gag gtt gaa ttc agg tgg ctc ttt cct ggg cag aag gac gaa agg cct Glu Val Glu Phe Arg Trp Leu Phe Pro Gly Gln Lys Asp Glu Arg Pro 305 310 315	1081
gtg acc atc cag gac acc tgg aga ctg att cac aga gga ctg gga cac Val Thr Ile Gln Asp Thr Trp Arg Leu Ile His Arg Gly Leu Gly His 320 325 330	1129

32600PWO.ST25.txt

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acc aca aga atc tcc cag agt gtc att atc gtg gaa gac ttt gag acc 1177
Thr Thr Arg Ile Ser Gln Ser Val Ile Ile Val Glu Asp Phe Glu Thr
335 340 345

att gat gcg ggc tac tac ata tgc aca gct cag aat ctc cga gga cag 1225
Ile Asp Ala Gly Tyr Tyr Ile Cys Thr Ala Gln Asn Leu Arg Gly Gln
350 355 360 365

acc aca gta gcg acc act gtt gag ttt tcc tga ttggaaagtg aagagtagtg 1278
Thr Thr Val Ala Thr Thr Val Glu Phe Ser
370 375

gaccaatggg atgcccatct gcacacacag cttccaggtg ctttatagga ggccaagggc 1338

caaccctctgc cagtgggtca gacagacatc cgaattaaaa ggaagtcact agtctattaa 1398

tagaagtata aactttccta actaaagtat gtatttttgac tcagccatgt ttctactttt 1458

tatactgaga aaacatgtca acaactttgt atcaatcgtt tctattaaat gagcaagatt 1518

ttataaaaaa aaaaaaaaaa aaaa 1542

```

```

<210> 35
<211> 375
<212> PRT
<213> Mus musculus

```

```
<400> 35
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```

Met Lys Phe Trp Leu Leu Leu Gly Leu Leu Leu Leu His Glu Ala Leu
1 5 10 15

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```

Glu Asp Val Ala Gly Gln His Ser Pro Lys Asn Lys Arg Pro Lys Glu
20 25 30

```

```

Gln Gly Glu Asn Arg Ile Lys Pro Thr Asn Lys Lys Ala Lys Pro Lys
35 40 45

```

```

Ile Pro Lys Val Lys Asp Arg Asp Ser Thr Asp Ser Thr Ala Lys Ser
50 55 60

```

```

Gln Ser Ile Met Met Gln Ala Met Gly Asn Gly Arg Phe Gln Arg Pro
65 70 75 80

```

```

Ala Ala Thr Val Ser Leu Leu Ala Gly Gln Thr Leu Glu Leu Arg Cys
85 90 95

```

```

Lys Gly Ser Lys Val Glu Trp Ser Tyr Pro Ala Tyr Leu Asp Thr Phe
100 105 110

```

```

Lys Asp Ser Arg Leu Thr Val Lys Gln Ser Glu Arg Tyr Gly Gln Leu
115 120 125

```

```

Thr Leu Val Asn Ser Thr Ala Ala Asp Thr Gly Glu Phe Ser Cys Trp
130 135 140

```

```
Glu Gln Leu Cys Asn Gly Tyr Ile Cys Arg Arg Asp Glu Ala Lys Thr
```

32600PWO.ST25.txt

```

145                150                155                160
Gly Ser Thr Tyr Ile Phe Phe Thr Glu Lys Gly Glu Leu Phe Val Pro
                165                170                175
Ser Pro Ser Tyr Phe Asp Val Val Tyr Leu Asn Pro Asp Arg Gln Ala
                180                185                190
Val Val Pro Cys Arg Val Thr Ala Pro Ser Ala Lys Val Thr Leu His
                195                200                205
Arg Glu Phe Pro Ala Lys Glu Ile Pro Ala Asn Gly Thr Asp Ile Val
                210                215                220
Tyr Asp Met Lys Arg Gly Phe Val Tyr Leu Gln Pro His Ser Asp His
                225                230                235
Gln Gly Val Val Tyr Cys Lys Ala Glu Ala Gly Gly Lys Ser Gln Ile
                245                250                255
Ser Val Lys Tyr Gln Leu Leu Tyr Val Glu Val Pro Ser Gly Pro Pro
                260                265                270
Ser Thr Thr Ile Leu Ala Ser Ser Asn Lys Val Arg Gly Gly Asp Asp
                275                280                285
Ile Ser Val Leu Cys Thr Val Leu Gly Glu Pro Asp Val Glu Val Glu
                290                295                300
Phe Arg Trp Leu Phe Pro Gly Gln Lys Asp Glu Arg Pro Val Thr Ile
                305                310                315
Gln Asp Thr Trp Arg Leu Ile His Arg Gly Leu Gly His Thr Thr Arg
                325                330                335
Ile Ser Gln Ser Val Ile Ile Val Glu Asp Phe Glu Thr Ile Asp Ala
                340                345                350
Gly Tyr Tyr Ile Cys Thr Ala Gln Asn Leu Arg Gly Gln Thr Thr Val
                355                360                365
Ala Thr Thr Val Glu Phe Ser
                370                375

```

```

<210> 36
<211> 1502
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (62)..(1189)

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<223> SF07, cDNA: NM_006207, Protein: NP_006198

<400> 36

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cctgcgtccc cgccccgcgc agccgcgcgc ctccctgcgct ccgagggtccg aggtttcccga      60
g atg aag gtc tgg ctg ctg ctt ggt ctt ctg ctg gtg cac gaa gcg ctg      109
  Met Lys Val Trp Leu Leu Leu Gly Leu Leu Leu Val His Glu Ala Leu
    1         5             10             15

gag gat gtt act ggc caa cac ctt ccc aag aac aag cgt cca aaa gaa      157
Glu Asp Val Thr Gly Gln His Leu Pro Lys Asn Lys Arg Pro Lys Glu
          20             25             30

cca gga gag aat aga atc aaa cct acc aac aag aag gtg aag ccc aaa      205
Pro Gly Glu Asn Arg Ile Lys Pro Thr Asn Lys Lys Val Lys Pro Lys
          35             40             45

att cct aaa atg aag gac agg gac tca gcc aat tca gca cca aag acg      253
Ile Pro Lys Met Lys Asp Arg Asp Ser Ala Asn Ser Ala Pro Lys Thr
          50             55             60

cag tct atc atg atg caa gtg ctg gat aaa ggt cgc ttc cag aaa ccc      301
Gln Ser Ile Met Met Gln Val Leu Asp Lys Gly Arg Phe Gln Lys Pro
          65             70             75             80

gcc gct acc ctg agt ctg ctg gcg ggg caa act gta gag ctt cga tgt      349
Ala Ala Thr Leu Ser Leu Leu Ala Gly Gln Thr Val Glu Leu Arg Cys
          85             90             95

aaa ggg agt aga att ggg tgg agc tac cct gcg tat ctg gac acc ttt      397
Lys Gly Ser Arg Ile Gly Trp Ser Tyr Pro Ala Tyr Leu Asp Thr Phe
          100            105            110

aag gat tct cgc ctc agc gtc aag cag aat gag cgc tac ggc cag ttg      445
Lys Asp Ser Arg Leu Ser Val Lys Gln Asn Glu Arg Tyr Gly Gln Leu
          115            120            125

act ctg gtc aac tcc acc tcg gca gac aca ggt gaa ttc agc tgc tgg      493
Thr Leu Val Asn Ser Thr Ser Ala Asp Thr Gly Glu Phe Ser Cys Trp
          130            135            140

gtg cag ctc tgc agc ggc tac atc tgc agg aag gac gag gcc aaa acg      541
Val Gln Leu Cys Ser Gly Tyr Ile Cys Arg Lys Asp Glu Ala Lys Thr
          145            150            155            160

ggc tcc acc tac atc ttt ttt aca gag aaa gga gaa ctc ttt gta cct      589
Gly Ser Thr Tyr Ile Phe Phe Thr Glu Lys Gly Glu Leu Phe Val Pro
          165            170            175

tct ccc agc tac ttc gat gtt gtc tac ttg aac ccg gac aga cag gct      637
Ser Pro Ser Tyr Phe Asp Val Val Tyr Leu Asn Pro Asp Arg Gln Ala
          180            185            190

gtg gtt cct tgt cgg gtg acc gtg ctg tcg gcc aaa gtc acg ctc cac      685
Val Val Pro Cys Arg Val Thr Val Leu Ser Ala Lys Val Thr Leu His
          195            200            205

agg gaa ttc cca gcc aag gag atc cca gcc aat gga acg gac att gtt      733
Arg Glu Phe Pro Ala Lys Gly Ile Pro Ala Asn Gly Thr Asp Ile Val
          210            215            220

tat gac atg aag cgg ggc ttt gtg tat ctg caa cct cat tcc gag cac      781
Tyr Asp Met Lys Arg Gly Phe Val Tyr Leu Gln Pro His Ser Glu His
          225            230            235            240

cag ggt gtg gtt tac tgc agg gcg gag gcc ggg ggc aga tct cag atc      829
Gln Gly Val Val Tyr Cys Arg Ala Glu Ala Gly Gly Arg Ser Gln Ile
          245            250            255

```


32600PWO.ST25.txt

```

tcc gtc aag tac cag ctg ctc tac gtg gcg gtt ccc agt ggc cct ccc      877
Ser Val Lys Tyr Gln Leu Leu Tyr Val Ala Val Pro Ser Gly Pro Pro
                260                270

tca aca acc atc ttg gct tct tca aac aaa gtg aaa agt ggg gac gac      925
Ser Thr Thr Ile Leu Ala Ser Ser Asn Lys Val Lys Ser Gly Asp Asp
                275                285

atc agt gtg ctc tgc act gtc ctg ggg gag ccc gat gtg gag gtg gag      973
Ile Ser Val Leu Cys Thr Val Leu Gly Glu Pro Asp Val Glu Val Glu
                290                300

ttc acc tgg atc ttc cca ggg cag aag gat gaa agg cct gtg acg atc      1021
Phe Thr Trp Ile Phe Pro Gly Gln Lys Asp Glu Arg Pro Val Thr Ile
305                310                315                320

caa gac act tgg agg ttg atc cac aga gga ctg gga cac acc acg aga      1069
Gln Asp Thr Trp Arg Leu Ile His Arg Gly Leu Gly His Thr Thr Arg
                325                330                335

atc tcc cag agt gtc att aca gtg gaa gac ttc gag acg att gat gca      1117
Ile Ser Gln Ser Val Ile Thr Val Glu Asp Phe Glu Thr Ile Asp Ala
                340                345                350

gga tat tac att tgc act gct cag aat ctt caa gga cag acc aca gta      1165
Gly Tyr Tyr Ile Cys Thr Ala Gln Asn Leu Gln Gly Gln Thr Thr Val
355                360                365

gct acc act gtt gag ttt tcc tga cttggaaaag gaaatgtaat gaacttatgg      1219
Ala Thr Thr Val Glu Phe Ser
370                375

aaagcccatt tgtgtacaca gtcagctttg gggttccttt tattagtgtt ttgccagagg      1279

ctgatgtcaa gcaccacacc ccaaccccag cgtctcgtga gtccgaccca gacatccaaa      1339

ctaaaaggaa gtcatccagt ctattcacag aagtgttaac ttttctaaca gaaagcatga      1399

ttttgattgc ttacctacat acgtgttcct agttttttata catgtgtataa caattttata      1459

taatcaatca tttctattaa atgagcacgt ttttgtaaaa aat                        1502

```

```

<210> 37
<211> 375
<212> PRT
<213> Homo sapiens

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<400> 37
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Met Lys Val Trp Leu Leu Leu Gly Leu Leu Leu Val His Glu Ala Leu
1          5          10          15

```

```
Glu Asp Val Thr Gly Gln His Leu Pro Lys Asn Lys Arg Pro Lys Glu
20          25          30

```

```
Pro Gly Glu Asn Arg Ile Lys Pro Thr Asn Lys Lys Val Lys Pro Lys
35          40          45

```

```
Ile Pro Lys Met Lys Asp Arg Asp Ser Ala Asn Ser Ala Pro Lys Thr
50          55          60

```

```
Gln Ser Ile Met Met Gln Val Leu Asp Lys Gly Arg Phe Gln Lys Pro

```

```

65              70              75              80
Ala Ala Thr Leu Ser Leu Leu Ala Gly Gln Thr Val Glu Leu Arg Cys
      85              90              95
Lys Gly Ser Arg Ile Gly Trp Ser Tyr Pro Ala Tyr Leu Asp Thr Phe
      100             105             110
Lys Asp Ser Arg Leu Ser Val Lys Gln Asn Glu Arg Tyr Gly Gln Leu
      115             120             125
Thr Leu Val Asn Ser Thr Ser Ala Asp Thr Gly Glu Phe Ser Cys Trp
      130             135             140
Val Gln Leu Cys Ser Gly Tyr Ile Cys Arg Lys Asp Glu Ala Lys Thr
      145             150             155             160
Gly Ser Thr Tyr Ile Phe Phe Thr Glu Lys Gly Glu Leu Phe Val Pro
      165             170             175
Ser Pro Ser Tyr Phe Asp Val Val Tyr Leu Asn Pro Asp Arg Gln Ala
      180             185             190
Val Val Pro Cys Arg Val Thr Val Leu Ser Ala Lys Val Thr Leu His
      195             200             205
Arg Glu Phe Pro Ala Lys Glu Ile Pro Ala Asn Gly Thr Asp Ile Val
      210             215             220
Tyr Asp Met Lys Arg Gly Phe Val Tyr Leu Gln Pro His Ser Glu His
      225             230             235             240
Gln Gly Val Val Tyr Cys Arg Ala Glu Ala Gly Gly Arg Ser Gln Ile
      245             250             255
Ser Val Lys Tyr Gln Leu Leu Tyr Val Ala Val Pro Ser Gly Pro Pro
      260             265             270
Ser Thr Thr Ile Leu Ala Ser Ser Asn Lys Val Lys Ser Gly Asp Asp
      275             280             285
Ile Ser Val Leu Cys Thr Val Leu Gly Glu Pro Asp Val Glu Val Glu
      290             295             300
Phe Thr Trp Ile Phe Pro Gly Gln Lys Asp Glu Arg Pro Val Thr Ile
      305             310             315             320
Gln Asp Thr Trp Arg Leu Ile His Arg Gly Leu Gly His Thr Thr Arg
      325             330             335
Ile Ser Gln Ser Val Ile Thr Val Glu Asp Phe Glu Thr Ile Asp Ala
      50

```

340

345

350

Gly Tyr Tyr Ile Cys Thr Ala Gln Asn Leu Gln Gly Gln Thr Thr Val
 355 360 365

Ala Thr Thr Val Glu Phe Ser
 370 375

<210> 38
 <211> 2379
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (69)..(2237)
 <223> SF08, cDNA: NM_019696, Protein: NP_062670

<400> 38
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 ttcccgcgt atg tgg ggt ctc ttg ctc gca gtg acc gcc ttt gcg cct tcc 110
 Met Trp Gly Leu Leu Leu Ala Val Thr Ala Phe Ala Pro Ser
 1 5 10
 gtc ggt ctg ggg ctg ggg gct ccc agc gcc tca gtg ccg ggc ctg gcg 158
 Val Gly Leu Gly Leu Gly Ala Pro Ser Ala Ser Val Pro Gly Leu Ala
 15 20 25 30
 ccg ggc tca acc ctg gct cca cac agc agc gtt gca cag ccg tcc aca 206
 Pro Gly Ser Thr Leu Ala Pro His Ser Ser Val Ala Gln Pro Ser Thr
 35 40 45
 aag gca aat gag acc tca gaa cgg cat gtc cgg ctt cga gtc atc aag 254
 Lys Ala Asn Glu Thr Ser Glu Arg His Val Arg Leu Arg Val Ile Lys
 50 55 60
 aaa aaa aag atc gtt gtc aag aag cga aag aag cta agg cac cct ggt 302
 Lys Lys Lys Ile Val Val Lys Lys Arg Lys Lys Leu Arg His Pro Gly
 65 70 75
 ccc ttg ggg act gct agg cct gtg gtg ccc act cac cca gca aag acc 350
 Pro Leu Gly Thr Ala Arg Pro Val Val Pro Thr His Pro Ala Lys Thr
 80 85 90
 ctc act ctc cct gag aaa caa gaa cca gga tgt ccc cct cta ggc ttg 398
 Leu Thr Leu Pro Glu Lys Gln Glu Pro Gly Cys Pro Pro Leu Gly Leu
 95 100 105 110
 gag tcc ttg agg gtt tca gat agc cag ctg gag gcc tcc agc agc cag 446
 Glu Ser Leu Arg Val Ser Asp Ser Gln Leu Glu Ala Ser Ser Ser Gln
 115 120 125
 tcc ttt ggt ctt gga gca cac cga gga cgg ctc aat atc cag tca ggt 494
 Ser Phe Gly Leu Gly Ala His Arg Gly Arg Leu Asn Ile Gln Ser Gly
 130 135 140
 ctg gag gac ggt gac ctg tat gat ggc gct tgg tgc gct gag caa caa 542
 Leu Glu Asp Gly Asp Leu Tyr Asp Gly Ala Trp Cys Ala Glu Gln Gln
 145 150 155
 gac act gaa cct tgg ctt cag gtg gat gca aag aat ccc gtc cgc ttc 590
 Asp Thr Glu Pro Trp Leu Gln Val Asp Ala Lys Asn Pro Val Arg Phe
 160 165 170

32600PWO.ST25.txt

gca gga att gtt aca cag ggc aga aac tct gtg tgg agg tat gac tgg Ala Gly Ile Val Thr Gln Gly Arg Asn Ser Val Trp Arg Tyr Asp Trp 175 180 185 190	638
gtc aca tca ttc aag gtc cag ttc agc aat gac agc cag acc tgg tgg Val Thr Ser Phe Lys Val Gln Phe Ser Asn Asp Ser Gln Thr Trp Trp 195 200 205	686
aag agt agg aac agt act gga atg gac ata gta ttt cct gcc aat tca Lys Ser Arg Asn Ser Thr Gly Met Asp Ile Val Phe Pro Ala Asn Ser 210 215 220	734
gac gca gag acc cca gtg ttg aac ctt ctg cca gag cct cag gtg gct Asp Ala Glu Thr Pro Val Leu Asn Leu Leu Pro Glu Pro Gln Val Ala 225 230 235	782
cga ttc att cgc ctg ctg cct cag acc tgg ttt cag gga ggt gta cct Arg Phe Ile Arg Leu Leu Pro Gln Thr Trp Phe Gln Gly Gly Val Pro 240 245 250	830
tgc ctc cgg gca gag atc ctg gcc tgc cca gtc tca gat cct aat gac Cys Leu Arg Ala Glu Ile Leu Ala Cys Pro Val Ser Asp Pro Asn Asp 255 260 265 270	878
ctg ttc cct gag gcc cac aca ctg gga tct tcg aac tct ttg gac ttc Leu Phe Pro Glu Ala His Thr Leu Gly Ser Asn Ser Leu Asp Phe 275 280 285	926
cgg cat cac aat tat aaa gct atg aga aag ctg atg aaa cag gtg aat Arg His His Asn Tyr Lys Ala Met Arg Lys Leu Met Lys Gln Val Asn 290 295 300	974
gag cag tgc ccc aac atc acg cgc atc tac agc atc ggg aag agc cac Glu Gln Cys Pro Asn Ile Thr Arg Ile Tyr Ser Ile Gly Lys Ser His 305 310 315	1022
cag ggt ttg aag ctg tat gtg atg gaa atg tca gac cat cct ggg gag Gln Gly Leu Lys Leu Tyr Val Met Glu Met Ser Asp His Pro Gly Glu 320 325 330	1070
cat gag ctg ggc gag ccc gag gtc cgc tac gtg gct gga atg cat ggg His Glu Leu Gly Glu Pro Glu Val Arg Tyr Val Ala Gly Met His Gly 335 340 345 350	1118
aat gag gcc ctg ggg cgg gag ttg ctt ctg ctt ttg atg cag ttc tta Asn Glu Ala Leu Gly Arg Glu Leu Leu Leu Leu Met Gln Phe Leu 355 360 365	1166
tgc cat gag ttc ctg cga ggg gac ccg cga gtg act cgg ctg ctc act Cys His Glu Phe Leu Arg Gly Asp Pro Arg Val Thr Arg Leu Leu Thr 370 375 380	1214
gag aca cga atc cat cta ttg ccc tcc atg aat cct gat ggc tat gag Glu Thr Arg Ile His Leu Leu Pro Ser Met Asn Pro Asp Gly Tyr Glu 385 390 395	1262
act gcc tac cac agg ggc tca gag ctg gtg ggc tgg gca gag ggc cgc Thr Ala Tyr His Arg Gly Ser Glu Leu Val Gly Trp Ala Glu Gly Arg 400 405 410	1310
tgg acc cac cag ggc att gac ctt aac cac aat ttt gct gac ctc aac Trp Thr His Gln Gly Ile Asp Leu Asn His Asn Phe Ala Asp Leu Asn 415 420 425 430	1358
aca caa ctg tgg tat gca gag gat gat gga ctg gta ccc gac act gtc Thr Gln Leu Trp Tyr Ala Glu Asp Asp Gly Leu Val Pro Asp Thr Val 435 440 445	1406

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ccc aac cat cac ctg cca ctg cct acc tac tat aca ttg ccc aat gcc	1454
Pro Asn His His Leu Pro Leu Pro Thr Tyr Tyr Thr Leu Pro Asn Ala	
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acc gtg gct cct gaa acg tgg gca gtg atc aaa tgg atg aag cgc atc	1502
Thr Val Ala Pro Glu Thr Trp Ala Val Ile Lys Trp Met Lys Arg Ile	
465 470 475	
ccg ttt gtg ctg agt gcc aac ctc cat ggg ggc gag ctt gtg gtg tcc	1550
Pro Phe Val Leu Ser Ala Asn Leu His Gly Gly Glu Leu Val Val Ser	
480 485 490	
tat cct ttc gac atg act cgg act ccg tgg gct gct cgt gaa ctc act	1598
Tyr Pro Phe Asp Met Thr Arg Thr Pro Trp Ala Ala Arg Glu Leu Thr	
495 500 505 510	
ccc aca cca gat gat gct gtc ttc cgc tgg ctc agc act gtc tat gct	1646
Pro Thr Pro Asp Asp Ala Val Phe Arg Trp Leu Ser Thr Val Tyr Ala	
515 520 525	
ggc acg aat agg gcc atg cag gat acc gac cgc cga cct tgt cat agc	1694
Gly Thr Asn Arg Ala Met Gln Asp Thr Asp Arg Arg Pro Cys His Ser	
530 535 540	
cag gac ttc tcc ttg cat ggc aac gtc atc aat gga gcc gac tgg cac	1742
Gln Asp Phe Ser Leu His Gly Asn Val Ile Asn Gly Ala Asp Trp His	
545 550 555	
aca gtt cct ggg agc atg aac gac ttc agc tac cta cac acc aat tgc	1790
Thr Val Pro Gly Ser Met Asn Asp Phe Ser Tyr Leu His Thr Asn Cys	
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ttt gag gtc aca gtg gag ctg tcc tgt gac aag ttc cct cat gag aag	1838
Phe Glu Val Thr Val Glu Leu Ser Cys Asp Lys Phe Pro His Glu Lys	
575 580 585 590	
gag ctg cct cag gag tgg gaa aac aac aaa gat gct ctt ctc acc tac	1886
Glu Leu Pro Gln Glu Trp Glu Asn Asn Lys Asp Ala Leu Leu Thr Tyr	
595 600 605	
ctg gag cag gtg cgc atg ggc att act gga gtt gtc cgg gat aaa gac	1934
Leu Glu Gln Val Arg Met Gly Ile Thr Gly Val Val Arg Asp Lys Asp	
610 615 620	
aca gag ctc ggc att gcg gat gct gtc att gcc gtg gag ggc att aac	1982
Thr Glu Leu Gly Ile Ala Asp Ala Val Ile Ala Val Glu Gly Ile Asn	
625 630 635	
cac gat gtt aca aca gct tgg ggc gga gat tac tgg cgg ctg ctg aca	2030
His Asp Val Thr Thr Ala Trp Gly Gly Asp Tyr Trp Arg Leu Leu Thr	
640 645 650	
cct ggg gac tat gtg gtg aca gcc agt gct gag ggt tac cat aca gtc	2078
Pro Gly Asp Tyr Val Val Thr Ala Ser Ala Glu Gly Tyr His Thr Val	
655 660 665 670	
aga caa cac tgt cag gtc acc ttt gaa gag ggc cct gtt ccc tgc aat	2126
Arg Gln His Cys Gln Val Thr Phe Glu Glu Gly Pro Val Pro Cys Asn	
675 680 685	
ttc cta ctc acc aag act ccc aaa gag agg ctt cga gaa ctg ttg gca	2174
Phe Leu Leu Thr Lys Thr Pro Lys Glu Arg Leu Arg Glu Leu Leu Ala	
690 695 700	
aca cga ggg aag ttg ccc cca gac ctt cgg agg aag ctg gag cgg ctg	2222
Thr Arg Gly Lys Leu Pro Pro Asp Leu Arg Arg Lys Leu Glu Arg Leu	
705 710 715	

agg gga cag aag taa cgtcttcagc tgaagagagc cacatccttg gacaggctgg 2277
 Arg Gly Gln Lys
 720

acctgtccag aactgaagga ggaggggggaa gagagagggga cggggtagaa gaggtgctct 2337

ggctcattaa agcttcgtgg tgcctgataa aaaaaaaaaa aa 2379

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 <213> Mus musculus

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Ser Thr Leu Ala Pro His Ser Ser Val Ala Gln Pro Ser Thr Lys Ala
 35 40 45

Asn Glu Thr Ser Glu Arg His Val Arg Leu Arg Val Ile Lys Lys Lys
 50 55 60

Lys Ile Val Val Lys Lys Arg Lys Lys Leu Arg His Pro Gly Pro Leu
 65 70 75 80

Gly Thr Ala Arg Pro Val Val Pro Thr His Pro Ala Lys Thr Leu Thr
 85 90 95

Leu Pro Glu Lys Gln Glu Pro Gly Cys Pro Pro Leu Gly Leu Glu Ser
 100 105 110

Leu Arg Val Ser Asp Ser Gln Leu Glu Ala Ser Ser Ser Gln Ser Phe
 115 120 125

Gly Leu Gly Ala His Arg Gly Arg Leu Asn Ile Gln Ser Gly Leu Glu
 130 135 140

Asp Gly Asp Leu Tyr Asp Gly Ala Trp Cys Ala Glu Gln Gln Asp Thr
 145 150 155 160

Glu Pro Trp Leu Gln Val Asp Ala Lys Asn Pro Val Arg Phe Ala Gly
 165 170 175

Ile Val Thr Gln Gly Arg Asn Ser Val Trp Arg Tyr Asp Trp Val Thr
 180 185 190

Ser Phe Lys Val Gln Phe Ser Asn Asp Ser Gln Thr Trp Trp Lys Ser
 195 200 205

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Arg Asn Ser Thr Gly Met Asp Ile Val Phe Pro Ala Asn Ser Asp Ala
 210 215 220
 Glu Thr Pro Val Leu Asn Leu Leu Pro Glu Pro Gln Val Ala Arg Phe
 225 230 235 240
 Ile Arg Leu Leu Pro Gln Thr Trp Phe Gln Gly Gly Val Pro Cys Leu
 245 250 255
 Arg Ala Glu Ile Leu Ala Cys Pro Val Ser Asp Pro Asn Asp Leu Phe
 260 265 270
 Pro Glu Ala His Thr Leu Gly Ser Ser Asn Ser Leu Asp Phe Arg His
 275 280 285
 His Asn Tyr Lys Ala Met Arg Lys Leu Met Lys Gln Val Asn Glu Gln
 290 295 300
 Cys Pro Asn Ile Thr Arg Ile Tyr Ser Ile Gly Lys Ser His Gln Gly
 305 310 315 320
 Leu Lys Leu Tyr Val Met Glu Met Ser Asp His Pro Gly Glu His Glu
 325 330 335
 Leu Gly Glu Pro Glu Val Arg Tyr Val Ala Gly Met His Gly Asn Glu
 340 345 350
 Ala Leu Gly Arg Glu Leu Leu Leu Leu Leu Met Gln Phe Leu Cys His
 355 360 365
 Glu Phe Leu Arg Gly Asp Pro Arg Val Thr Arg Leu Leu Thr Glu Thr
 370 375 380
 Arg Ile His Leu Leu Pro Ser Met Asn Pro Asp Gly Tyr Glu Thr Ala
 385 390 395 400
 Tyr His Arg Gly Ser Glu Leu Val Gly Trp Ala Glu Gly Arg Trp Thr
 405 410 415
 His Gln Gly Ile Asp Leu Asn His Asn Phe Ala Asp Leu Asn Thr Gln
 420 425 430
 Leu Trp Tyr Ala Glu Asp Asp Gly Leu Val Pro Asp Thr Val Pro Asn
 435 440 445
 His His Leu Pro Leu Pro Thr Tyr Tyr Thr Leu Pro Asn Ala Thr Val
 450 455 460
 Ala Pro Glu Thr Trp Ala Val Ile Lys Trp Met Lys Arg Ile Pro Phe
 465 470 475 480

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Val Leu Ser Ala Asn Leu His Gly Gly Glu Leu Val Val Ser Tyr Pro
485 490 495

Phe Asp Met Thr Arg Thr Pro Trp Ala Ala Arg Glu Leu Thr Pro Thr
500 505 510

Pro Asp Asp Ala Val Phe Arg Trp Leu Ser Thr Val Tyr Ala Gly Thr
515 520 525

Asn Arg Ala Met Gln Asp Thr Asp Arg Arg Pro Cys His Ser Gln Asp
530 535 540

Phe Ser Leu His Gly Asn Val Ile Asn Gly Ala Asp Trp His Thr Val
545 550 555 560

Pro Gly Ser Met Asn Asp Phe Ser Tyr Leu His Thr Asn Cys Phe Glu
565 570 575

Val Thr Val Glu Leu Ser Cys Asp Lys Phe Pro His Glu Lys Glu Leu
580 585 590

Pro Gln Glu Trp Glu Asn Asn Lys Asp Ala Leu Leu Thr Tyr Leu Glu
595 600 605

Gln Val Arg Met Gly Ile Thr Gly Val Val Arg Asp Lys Asp Thr Glu
610 615 620

Leu Gly Ile Ala Asp Ala Val Ile Ala Val Glu Gly Ile Asn His Asp
625 630 635 640

Val Thr Thr Ala Trp Gly Gly Asp Tyr Trp Arg Leu Leu Thr Pro Gly
645 650 655

Asp Tyr Val Val Thr Ala Ser Ala Glu Gly Tyr His Thr Val Arg Gln
660 665 670

His Cys Gln Val Thr Phe Glu Glu Gly Pro Val Pro Cys Asn Phe Leu
675 680 685

Leu Thr Lys Thr Pro Lys Glu Arg Leu Arg Glu Leu Leu Ala Thr Arg
690 695 700

Gly Lys Leu Pro Pro Asp Leu Arg Arg Lys Leu Glu Arg Leu Arg Gly
705 710 715 720

Gln Lys

<210> 40
<211> 2390
<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (65)..(2269)

<223> SF08, cDNA: NM_019609, Protein: NP_062555

<400> 40

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cgcc atg tgg ggg ctc ctg ctc gcc ctg gcc gcc ttc gcg ccg gcc gtc 109

Met Trp Gly Leu Leu Leu Ala Leu Ala Ala Phe Ala Pro Ala Val
1 5 10 15

ggc ccg gct ctg ggg gcg ccc agg aac tcg gtg ctg ggc ctc gcg cag 157

Gly Pro Ala Leu Gly Ala Pro Arg Asn Ser Val Leu Gly Leu Ala Gln
20 25 30

ccc ggg acc acc aag gtc cca ggc tcg acc ccg gcc ctg cat agc agc 205

Pro Gly Thr Thr Lys Val Pro Gly Ser Thr Pro Ala Leu His Ser Ser
35 40 45

ccg gca cag ccg ccg gcg gag aca gct aac ggg acc tca gaa cag cat 253

Pro Ala Gln Pro Pro Ala Glu Thr Ala Asn Gly Thr Ser Glu Gln His
50 55 60

gtc ccg att cga gtc atc aag aag aaa aag gtc att atg aag aag ccg 301

Val Arg Ile Arg Val Ile Lys Lys Lys Lys Val Ile Met Lys Lys Arg
65 70 75

aag aag cta act cta act cgc ccc acc cca ctg gtg act gcc ggg ccc 349

Lys Lys Leu Thr Leu Thr Arg Pro Thr Pro Leu Val Thr Ala Gly Pro
80 85 90 95

ctt gtg acc ccc act cca gca ggg acc ctc gac ccc gct gag aaa caa 397

Leu Val Thr Pro Thr Pro Ala Gly Thr Leu Asp Pro Ala Glu Lys Gln
100 105 110

gaa aca ggc tgt cct cct ttg ggt ctg gag tcc ctg cga gtt tca gat 445

Glu Thr Gly Cys Pro Pro Leu Gly Leu Glu Ser Leu Arg Val Ser Asp
115 120 125

agc ccg ctt gag gca tcc agc agc cag tcc ttt ggt ctt gga cca cac 493

Ser Arg Leu Glu Ala Ser Ser Ser Gln Ser Phe Gly Leu Gly Pro His
130 135 140

cga gga ccg ctc aac att cag tca ggc ctg gag gac ggc gat cta tat 541

Arg Gly Arg Leu Asn Ile Gln Ser Gly Leu Glu Asp Gly Asp Leu Tyr
145 150 155

gat gga gcc tgg tgt gct gag gag cag gac gcc gat cca tgg ttt cag 589

Asp Gly Ala Trp Cys Ala Glu Glu Gln Asp Ala Asp Pro Trp Phe Gln
160 165 170 175

gtg gac gct ggg cac ccc acc cgc ttc tcg ggt gtt atc aca cag ggc 637

Val Asp Ala Gly His Pro Thr Arg Phe Ser Gly Val Ile Thr Gln Gly
180 185 190

agg aac tct gtc tgg agg tat gac tgg gtc aca tca tac aag gtc cag 685

Arg Asn Ser Val Trp Arg Tyr Asp Trp Val Thr Ser Tyr Lys Val Gln
195 200 205

ttc agc aat gac agt ccg acc tgg tgg gga agt agg aac cac agc agt 733

Phe Ser Asn Asp Ser Arg Thr Trp Trp Gly Ser Arg Asn His Ser Ser
210 215 220

ggg atg gac gca gta ttt cct gcc aat tca gac cca gaa act cca gtg 781

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Gly	Met	Asp	Ala	Val	Phe	Pro	Ala	Asn	Ser	Asp	Pro	Glu	Thr	Pro	Val		
225						230					235						
ctg	aac	ctc	ctg	cgc	gag	ccc	cag	gtg	gcc	cgc	ttc	att	cgc	ctg	ctg	829	
Leu	Asn	Leu	Leu	Pro	Glu	Pro	Gln	Val	Ala	Arg	Phe	Ile	Arg	Leu	Leu		
240					245					250					255		
ccc	cag	acc	tgg	ctc	cag	gga	ggc	gcg	cct	tgc	ctc	cgg	gca	gag	atc	877	
Pro	Gln	Thr	Trp	Leu	Gln	Gly	Gly	Ala	Pro	Cys	Leu	Arg	Ala	Glu	Ile		
				260					265					270			
ctg	gcc	tgc	cca	gtc	tca	gac	ccc	aat	gac	cta	ttc	ctt	gag	gcc	cct	925	
Leu	Ala	Cys	Pro	Val	Ser	Asp	Pro	Asn	Asp	Leu	Phe	Leu	Glu	Ala	Pro		
			275					280					285				
gcg	tcg	gga	tcc	tct	gac	cct	cta	gac	ttt	cag	cat	cac	aat	tac	aag	973	
Ala	Ser	Gly	Ser	Ser	Asp	Pro	Leu	Asp	Phe	Gln	His	His	Asn	Tyr	Lys		
		290					295					300					
gcc	atg	agg	aag	ctg	atg	aag	cag	gta	caa	gag	caa	tgc	ccc	aac	atc	1021	
Ala	Met	Arg	Lys	Leu	Met	Lys	Gln	Val	Gln	Glu	Gln	Cys	Pro	Asn	Ile		
	305					310					315						
acc	cgc	atc	tac	agc	att	ggg	aag	agc	tac	cag	ggc	ctg	aag	ctg	tat	1069	
Thr	Arg	Ile	Tyr	Ser	Ile	Gly	Lys	Ser	Tyr	Gln	Gly	Leu	Lys	Leu	Tyr		
320					325					330					335		
gtg	atg	gaa	atg	tcg	gac	aag	cct	ggg	gag	cat	gag	ctg	ggg	gag	cct	1117	
Val	Met	Glu	Met	Ser	Asp	Lys	Pro	Gly	Glu	His	Glu	Leu	Gly	Glu	Pro		
				340					345					350			
gag	gtg	cgc	tac	gtg	gct	ggc	atg	cat	ggg	aac	gag	gcc	ctg	ggg	cgg	1165	
Glu	Val	Arg	Tyr	Val	Ala	Gly	Met	His	Gly	Asn	Glu	Ala	Leu	Gly	Arg		
			355					360					365				
gag	ttg	ctt	ctg	ctc	ctg	atg	cag	ttc	ctg	tgc	cat	gag	ttc	ctg	cga	1213	
Glu	Leu	Leu	Leu	Leu	Leu	Met	Gln	Phe	Leu	Cys	His	Glu	Phe	Leu	Arg		
		370					375					380					
ggg	aac	cca	cgg	gtg	acc	cgg	ctg	ctc	tct	gag	atg	cgc	att	cac	ctg	1261	
Gly	Asn	Pro	Arg	Val	Thr	Arg	Leu	Leu	Ser	Glu	Met	Arg	Ile	His	Leu		
	385					390					395						
ctg	ccc	tcc	atg	aac	cct	gat	ggc	tat	gag	atc	gcc	tac	cac	cgg	ggt	1309	
Leu	Pro	Ser	Met	Asn	Pro	Asp	Gly	Tyr	Glu	Ile	Ala	Tyr	His	Arg	Gly		
400					405					410					415		
tca	gag	ctg	gtg	ggc	tgg	gcc	gag	ggc	cgc	tgg	aac	aac	cag	agc	atc	1357	
Ser	Glu	Leu	Val	Gly	Trp	Ala	Glu	Gly	Arg	Trp	Asn	Asn	Gln	Ser	Ile		
				420					425					430			
gat	ctt	aac	cat	aat	ttt	gct	gac	ctc	aac	aca	cca	ctg	tgg	gaa	gca	1405	
Asp	Leu	Asn	His	Asn	Phe	Ala	Asp	Leu	Asn	Thr	Pro	Leu	Trp	Glu	Ala		
			435					440					445				
cag	gac	gat	ggg	aag	gtg	ccc	cac	atc	gtc	ccc	aac	cat	cac	ctg	cca	1453	
Gln	Asp	Asp	Gly	Lys	Val	Pro	His	Ile	Val	Pro	Asn	His	His	Leu	Pro		
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ttg	ccc	act	tac	tac	acc	ctg	ccc	aat	gcc	acc	gtg	gct	cct	gaa	acg	1501	
Leu	Pro	Thr	Tyr	Tyr	Thr	Leu	Pro	Asn	Ala	Thr	Val	Ala	Pro	Glu	Thr		
	465					470					475						
cgg	gca	gta	atc	aag	tgg	atg	aag	cgg	atc	ccc	ttt	gtg	cta	agt	gcc	1549	
Arg	Ala	Val	Ile	Lys	Trp	Met	Lys	Arg	Ile	Pro	Phe	Val	Leu	Ser	Ala		
480					485					490					495		
aac	ctc	cac	ggg	ggt	gag	ctc	gtg	gtg	tcc	tac	cca	ttc	gac	atg	act	1597	

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Asn	Leu	His	Gly	Gly	Glu	Leu	Val	Val	Ser	Tyr	Pro	Phe	Asp	Met	Thr	
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Arg	Thr	Pro	Trp	Ala	Ala	Arg	Glu	Leu	Thr	Pro	Thr	Pro	Asp	Asp	Ala	
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gtg	ttt	cgc	tgg	ctc	agc	act	gtc	tat	gct	ggc	agt	aat	ctg	gcc	atg	1693
Val	Phe	Arg	Trp	Leu	Ser	Thr	Val	Tyr	Ala	Gly	Ser	Asn	Leu	Ala	Met	
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cag	gac	acc	agc	cgc	cga	ccc	tgc	cac	agc	cag	gac	ttc	tcc	gtg	cac	1741
Gln	Asp	Thr	Ser	Arg	Arg	Pro	Cys	His	Ser	Gln	Asp	Phe	Ser	Val	His	
			545			550					555					
ggc	aac	atc	atc	aac	ggg	gct	gac	tgg	cac	acg	gtc	ccc	ggg	agc	atg	1789
Gly	Asn	Ile	Ile	Asn	Gly	Ala	Asp	Trp	His		Val	Pro	Gly	Ser	Met	
					565					570					575	
aat	gac	ttc	agc	tac	cta	cac	acc	aac	tgc	ttt	gag	gtc	act	gtg	gag	1837
Asn	Asp	Phe	Ser	Tyr	Leu	His	Thr	Asn	Cys	Phe	Glu	Val	Thr	Val	Glu	
				580					585					590		
ctg	tcc	tgt	gac	aag	ttc	cct	cac	gag	aat	gaa	ttg	ccc	cag	gag	tgg	1885
Leu	Ser	Cys	Asp	Lys	Phe	Pro	His	Glu	Asn	Glu	Leu	Pro	Gln	Glu	Trp	
			595					600					605			
gag	aac	aac	aaa	gac	gcc	ctc	ctc	acc	tac	ctg	gag	cag	gtg	cgc	atg	1933
Glu	Asn	Asn	Lys	Asp	Ala	Leu	Leu	Thr	Tyr	Leu	Glu	Gln	Val	Arg	Met	
			610				615					620				
ggc	att	gca	gga	gtg	gtg	agg	gac	aag	gac	acg	gag	ctt	ggg	att	gct	1981
Gly	Ile	Ala	Gly	Val	Val	Arg	Asp	Lys	Asp	Thr	Glu	Leu	Gly	Ile	Ala	
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gac	gct	gtc	att	gcc	gtg	gat	ggg	att	aac	cat	gac	gtg	acc	acg	gcg	2029
Asp	Ala	Val	Ile	Ala	Val	Asp	Gly	Ile	Asn	His	Asp	Val	Thr	Thr	Ala	
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Trp	Gly	Gly	Asp	Tyr	Trp	Arg	Leu	Leu	Thr	Pro	Gly	Asp	Tyr	Met	Val	
				660					665					670		
act	gcc	agt	gcc	gag	ggc	tac	cat	tca	gtg	aca	cgg	aac	tgt	cgg	gtc	2125
Thr	Ala	Ser	Ala	Glu	Gly	Tyr	His	Ser	Val	Thr	Arg	Asn	Cys	Arg	Val	
				675				680					685			
acc	ttt	gaa	gag	ggc	ccc	ttc	ccc	tgc	aat	ttc	gtg	ctc	acc	aag	act	2173
Thr	Phe	Glu	Glu	Gly	Pro	Phe	Pro	Cys	Asn	Phe	Val	Leu	Thr	Lys	Thr	
			690				695					700				
ccc	aaa	cag	agg	ctg	cgc	gag	ctg	ctg	gca	gct	ggg	gcc	aag	gtg	ccc	2221
Pro	Lys	Gln	Arg	Leu	Arg	Glu	Leu	Leu	Ala	Ala	Gly	Ala	Lys	Val	Pro	
			705			710					715					
ccg	gac	ctt	cgc	agg	cgc	ctg	gag	cgg	cta	agg	gga	cag	aag	gat	tga	2269
Pro	Asp	Leu	Arg	Arg	Arg	Leu	Glu	Arg	Leu	Arg	Gly	Gln	Lys	Asp		
					725				730							
tac	ctg	cggt	tta	agag	cccc	tag	ggc	cagg	tc	gac	ctg	tgc	aag	acg	ggg	2329
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a																2390

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<212> PRT

<213> Homo sapiens

<400> 41

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 35 40 45

Ala Gln Pro Pro Ala Glu Thr Ala Asn Gly Thr Ser Glu Gln His Val
 50 55 60

Arg Ile Arg Val Ile Lys Lys Lys Lys Val Ile Met Lys Lys Arg Lys
 65 70 75 80

Lys Leu Thr Leu Thr Arg Pro Thr Pro Leu Val Thr Ala Gly Pro Leu
 85 90 95

Val Thr Pro Thr Pro Ala Gly Thr Leu Asp Pro Ala Glu Lys Gln Glu
 100 105 110

Thr Gly Cys Pro Pro Leu Gly Leu Glu Ser Leu Arg Val Ser Asp Ser
 115 120 125

Arg Leu Glu Ala Ser Ser Ser Gln Ser Phe Gly Leu Gly Pro His Arg
 130 135 140

Gly Arg Leu Asn Ile Gln Ser Gly Leu Glu Asp Gly Asp Leu Tyr Asp
 145 150 155 160

Gly Ala Trp Cys Ala Glu Glu Gln Asp Ala Asp Pro Trp Phe Gln Val
 165 170 175

Asp Ala Gly His Pro Thr Arg Phe Ser Gly Val Ile Thr Gln Gly Arg
 180 185 190

Asn Ser Val Trp Arg Tyr Asp Trp Val Thr Ser Tyr Lys Val Gln Phe
 195 200 205

Ser Asn Asp Ser Arg Thr Trp Trp Gly Ser Arg Asn His Ser Ser Gly
 210 215 220

Met Asp Ala Val Phe Pro Ala Asn Ser Asp Pro Glu Thr Pro Val Leu
 225 230 235 240

Asn Leu Leu Pro Glu Pro Gln Val Ala Arg Phe Ile Arg Leu Leu Pro
 245 250 255

32600PWO.ST25.txt

Gln Thr Trp Leu Gln Gly Gly Ala Pro Cys Leu Arg Ala Glu Ile Leu
 260 265 270
 Ala Cys Pro Val Ser Asp Pro Asn Asp Leu Phe Leu Glu Ala Pro Ala
 275 280 285
 Ser Gly Ser Ser Asp Pro Leu Asp Phe Gln His His Asn Tyr Lys Ala
 290 295 300
 Met Arg Lys Leu Met Lys Gln Val Gln Glu Gln Cys Pro Asn Ile Thr
 305 310 315 320
 Arg Ile Tyr Ser Ile Gly Lys Ser Tyr Gln Gly Leu Lys Leu Tyr Val
 325 330 335
 Met Glu Met Ser Asp Lys Pro Gly Glu His Glu Leu Gly Glu Pro Glu
 340 345 350
 Val Arg Tyr Val Ala Gly Met His Gly Asn Glu Ala Leu Gly Arg Glu
 355 360 365
 Leu Leu Leu Leu Leu Met Gln Phe Leu Cys His Glu Phe Leu Arg Gly
 370 375 380
 Asn Pro Arg Val Thr Arg Leu Leu Ser Glu Met Arg Ile His Leu Leu
 385 390 395 400
 Pro Ser Met Asn Pro Asp Gly Tyr Glu Ile Ala Tyr His Arg Gly Ser
 405 410 415
 Glu Leu Val Gly Trp Ala Glu Gly Arg Trp Asn Asn Gln Ser Ile Asp
 420 425 430
 Leu Asn His Asn Phe Ala Asp Leu Asn Thr Pro Leu Trp Glu Ala Gln
 435 440 445
 Asp Asp Gly Lys Val Pro His Ile Val Pro Asn His His Leu Pro Leu
 450 455 460
 Pro Thr Tyr Tyr Thr Leu Pro Asn Ala Thr Val Ala Pro Glu Thr Arg
 465 470 475 480
 Ala Val Ile Lys Trp Met Lys Arg Ile Pro Phe Val Leu Ser Ala Asn
 485 490 495
 Leu His Gly Gly Glu Leu Val Val Ser Tyr Pro Phe Asp Met Thr Arg
 500 505 510
 Thr Pro Trp Ala Ala Arg Glu Leu Thr Pro Thr Pro Asp Asp Ala Val
 515 520 525

32600PWO.ST25.txt

Phe Arg Trp Leu Ser Thr Val Tyr Ala Gly Ser Asn Leu Ala Met Gln
530 535 540

Asp Thr Ser Arg Arg Pro Cys His Ser Gln Asp Phe Ser Val His Gly
545 550 555 560

Asn Ile Ile Asn Gly Ala Asp Trp His Thr Val Pro Gly Ser Met Asn
565 570 575

Asp Phe Ser Tyr Leu His Thr Asn Cys Phe Glu Val Thr Val Glu Leu
580 585 590

Ser Cys Asp Lys Phe Pro His Glu Asn Glu Leu Pro Gln Glu Trp Glu
595 600 605

Asn Asn Lys Asp Ala Leu Leu Thr Tyr Leu Glu Gln Val Arg Met Gly
610 615 620

Ile Ala Gly Val Val Arg Asp Lys Asp Thr Glu Leu Gly Ile Ala Asp
625 630 635 640

Ala Val Ile Ala Val Asp Gly Ile Asn His Asp Val Thr Thr Ala Trp
645 650 655

Gly Gly Asp Tyr Trp Arg Leu Leu Thr Pro Gly Asp Tyr Met Val Thr
660 665 670

Ala Ser Ala Glu Gly Tyr His Ser Val Thr Arg Asn Cys Arg Val Thr
675 680 685

Phe Glu Glu Gly Pro Phe Pro Cys Asn Phe Val Leu Thr Lys Thr Pro
690 695 700

Lys Gln Arg Leu Arg Glu Leu Leu Ala Ala Gly Ala Lys Val Pro Pro
705 710 715 720

Asp Leu Arg Arg Arg Leu Glu Arg Leu Arg Gly Gln Lys Asp
725 730

<210> 42
<211> 1815
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (98)..(535)
<223> SF09, cDNA: NM_139295, Protein: NP_647456

<400> 42
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actgcgtcgg ggattatcgg ggtacccacc cggaagc atg gca acc cta cag ctg 115
62

32600PWO.ST25.txt

Met Ala Thr Leu Gln Leu
1 5

ctc aga gct ccc ttg ctg tgt gtc ctg ctt tgg gtc ttt tgt gct cca	163
Leu Arg Ala Pro Leu Leu Cys Val Leu Leu Trp Val Phe Cys Ala Pro	
10 15 20	
ggc gcc aga gcc cat gac cat ggg gct gat gtc cat cat ggc agc gtg	211
Gly Ala Arg Ala His Asp His Gly Ala Asp Val His His Gly Ser Val	
25 30 35	
ggc ctg gat aag agc aca gtg cac gac caa gag cac atc atg gaa cat	259
Gly Leu Asp Lys Ser Thr Val His Asp Gln Glu His Ile Met Glu His	
40 45 50	
ctg gaa ggt gtc atc gac cag cca gag gcg gag atg tcc cca cag gaa	307
Leu Glu Gly Val Ile Asp Gln Pro Glu Ala Glu Met Ser Pro Gln Glu	
55 60 65 70	
ctg cag ctc cat tac ttc aaa atg cat gat tac gac ggc aac agt ttg	355
Leu Gln Leu His Tyr Phe Lys Met His Asp Tyr Asp Gly Asn Ser Leu	
75 80 85	
ctt gac ggc cta gag ctc tcc ata gcc atc act cac gtg cac aag gag	403
Leu Asp Gly Leu Glu Leu Ser Ile Ala Ile Thr His Val His Lys Glu	
90 95 100	
gag ggg agt gag cag gcg cca gtc atg agc gag gat gag ctc gtc agc	451
Glu Gly Ser Glu Gln Ala Pro Val Met Ser Glu Asp Glu Leu Val Ser	
105 110 115	
atc ata gat ggt gtc ctg agg gac gat gac aag aac aat gac ggc tac	499
Ile Ile Asp Gly Val Leu Arg Asp Asp Asp Lys Asn Asn Asp Gly Tyr	
120 125 130	
atc gac tac gct gag ttt gca aag tca ctg cag tag accgttggct	545
Ile Asp Tyr Ala Glu Phe Ala Lys Ser Leu Gln	
135 140 145	
ctttcctttg tgcacatgtg acccttgcta atgtgatgga cgtgtctggg aatgcgaaac	605
aacttatcttc cgtctactgc tcagcacttt ggtaagagcc tgtggcagtc tgtaagagtg	665
gggtgaggaa gaagccacat gactgtggag agaagtggga caggcctcag tccctagagg	725
tgtgtttaag cttgttgggc aagagccgga tgcggatctt cggaagggcg gtgggtatcc	785
cgagttctca ggaatccgac tgtagaatgc cactctgact tcttgatgtt aatccatgct	845
acctaaagta aagacaggct gcttggccaa gtggacacac ttgagaaaca gtggagggag	905
agtgtgaaag ccacacgctt gccctgggtg gtctgtgtct taggcagatg tggtcagtat	965
tctgttcccc aggcatacag catcatatat taaagccaca gcagaagagg aatgtcgccc	1025
actgaggcca cccagatgca gactctagga ttccttgccc actggccttt tggaaatgaa	1085
gcaccactgg cctgaataat tagcattttc cagatcttca gtatcttcca caactactgc	1145
cataccctgt gttgtatcat ttgaccagga gggaaacctt gaattggggg gtgttctcta	1205
atcactttcc actgtctgag ctttcctgac ccctgtattg tctccttgct cccagggctc	1265
ccttcatggc ttgtgaactg ttaacttggg atctcagggt aaactgtcag ctgggtctagc	1325
ctgagcgagg cctgagacca tcagtcacta agagcagtgg ctaacctcat cgaagtggga	1385
aggaatgttt ttaaaattac ctcttcgagc ctgaatacaa agaataaaaag aataaaaagaa	1445

32600PWO.ST25.txt

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ttctttttaat ttcaggggaag atcagaaaaag aaagcctaaa gccctttagc gttgtgaacc 1505
tcagtagtag ctgaaagaga agctgccaca ggttgtactt gctctgtgag atgttgtaga 1565
cattccgtaa gagaatccag aatgatagca ggatcaggaa agaaatggag ccaaatctgc 1625
tctaaggtga atagagactt atttttcttt attaaagtat tcttgtaaga cagttttctg 1685
tgtcaagtat ttgtgaaatc agagctgaca tgtaagctat tcttgtaata tctcattatt 1745
ttgaaagatt tatataatga actctggcta tctgacaata aaatggatga aaaagcaaaa 1805
aaaaaaaaaa 1815

```

```

<210> 43
<211> 145
<212> PRT
<213> Mus musculus

```

```
<400> 43
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```

Met Ala Thr Leu Gln Leu Leu Arg Ala Pro Leu Leu Cys Val Leu Leu
1          5          10          15

```

```

Trp Val Phe Cys Ala Pro Gly Ala Arg Ala His Asp His Gly Ala Asp
          20          25          30

```

```

Val His His Gly Ser Val Gly Leu Asp Lys Ser Thr Val His Asp Gln
          35          40          45

```

```

Glu His Ile Met Glu His Leu Glu Gly Val Ile Asp Gln Pro Glu Ala
          50          55          60

```

```

Glu Met Ser Pro Gln Glu Leu Gln Leu His Tyr Phe Lys Met His Asp
65          70          75          80

```

```

Tyr Asp Gly Asn Ser Leu Leu Asp Gly Leu Glu Leu Ser Ile Ala Ile
          85          90          95

```

```

Thr His Val His Lys Glu Glu Gly Ser Glu Gln Ala Pro Val Met Ser
          100          105          110

```

```

Glu Asp Glu Leu Val Ser Ile Ile Asp Gly Val Leu Arg Asp Asp Asp
          115          120          125

```

```

Lys Asn Asn Asp Gly Tyr Ile Asp Tyr Ala Glu Phe Ala Lys Ser Leu
          130          135          140

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```

Gln
145

```

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<210> 44
<211> 4144
<212> DNA
<213> Homo sapiens

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32600PWO.ST25.txt

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<220>
<221> CDS
<222> (95)..(535)
<223> SF09, cDNA: NM_139279, Protein: NP_644808

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cttcgcgtct gcttcggaga ccgtaaggat attg atg acc atg aga tcc ctg ctc 115
Met Thr Met Arg Ser Leu Leu
1 5

aga acc ccc ttc ctg tgt ggc ctg ctc tgg gcc ttt tgt gcc cca ggc 163
Arg Thr Pro Phe Leu Cys Gly Leu Leu Trp Ala Phe Cys Ala Pro Gly
10 15 20

gcc agg gct gag gag cct gca gcc agc ttc tcc caa ccc ggc agc atg 211
Ala Arg Ala Glu Glu Pro Ala Ala Ser Phe Ser Gln Pro Gly Ser Met
25 30 35

ggc ctg gat aag aac aca gtg cac gac caa gag cat atc atg gag cat 259
Gly Leu Asp Lys Asn Thr Val His Asp Gln Glu His Ile Met Glu His
40 45 50 55

cta gaa ggt gtc atc aac aaa cca gag gcg gag atg tcg cca caa gaa 307
Leu Glu Gly Val Ile Asn Lys Pro Glu Ala Glu Met Ser Pro Gln Glu
60 65 70

ttg cag ctc cat tac ttc aaa atg cat gat tat gat ggc aat aat ttg 355
Leu Gln Leu His Tyr Phe Lys Met His Asp Tyr Asp Gly Asn Asn Leu
75 80 85

ctt gat ggc tta gaa ctc tcc aca gcc atc act cat gtc cat aag gag 403
Leu Asp Gly Leu Glu Leu Ser Thr Ala Ile Thr His Val His Lys Glu
90 95 100

gaa ggg agt gaa cag gca cca cta atg agt gaa gat gaa ctg att aac 451
Glu Gly Ser Glu Gln Ala Pro Leu Met Ser Glu Asp Glu Leu Ile Asn
105 110 115

ata ata gat ggt gtt ttg aga gat gat gac aag aac aat gat gga tac 499
Ile Ile Asp Gly Val Leu Arg Asp Asp Asp Lys Asn Asn Asp Gly Tyr
120 125 130 135

att gac tat gct gaa ttt gca aaa tca ctg cag tag atgttatttg 545
Ile Asp Tyr Ala Glu Phe Ala Lys Ser Leu Gln
140 145

gccatctcct gggttatatac aaatgtgacc cgtgataatg tgattgaaca ctttagtaat 605
gcaaaataac tcattttccaa ctactgctgc agcatttttg taaaaacctg tagcgattcg 665
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ttcttacatg gcagcaagag aaaatgagga agaagcaaaa gtggaaaccc ctgataagcc 965
atcagatctt gtgaaactta ttcactatca caagaatagc atgggaaaga ctggccccc 1025
tgattcaatt acctccctt ggggtctctc cacaacacgt gggaattctg gtagatacaa 1085
tttcaagttg agatttgggt ggggacatag ccaaaccata tcattctacc cctggcccct 1145

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32600PWO.ST25.txt

ccaaatctca	tgtcctcact	attcaaaaacc	aatcatgcct	tcctaacagt	cccccaaagt	1205
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caagtccctt	ccacctatga	gcctgtaaaa	tcaaaagcaa	gctagttact	tcctagatac	1325
caacaggggt	acaggtattg	attaaagacg	gctgttccaa	atgggagaaa	ttggccaaaa	1385
taaaggggtt	acagggccca	tgcaagtccg	aatccagca	gggctgtcaa	attttaaagt	1445
tccagaataa	tctcctttga	ctccaggtct	cacatccagg	tcatactgat	gcaagaagtg	1505
ggttcccatg	gtcttgggca	gctctgcccc	tgtggctttg	tagggtagac	cctccctcct	1565
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tatgcaaatt	tctgcagctg	gcttgaattt	ctcccagaa	aatgggtttt	tcttttctat	2165
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cagcatttgg	ggcaaagcca	ttcaacaagt	ctgtaggaag	ttccaaactt	tcccacattt	2525
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gtcacttcca	cattttgggt	atttcttcag	caggtcccaa	tctactggta	ccaatttact	2645
gtattagtcc	gttttcacgc	tgctgataaa	gacatacccg	agactgggaa	gaaaaagtgg	2705
tttaattgga	cttaaagttc	cacatggctg	gggaggcctc	agaatcatgg	tgggaggcaa	2765
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ataaactgat	cagatctcat	gagacttatt	cactgtcacg	agaatagcac	gggaaagact	2885
ggcccccatg	attcaattac	ctccccctgg	gtctgtccca	caacacgtgg	gaattctggg	2945
agatacaatt	caagttgaga	tttggtgggg	gacacaacca	aaccatatca	gcctcctttc	3005
aagaatatta	gataattgga	gctgagtact	caggaacttg	actgtagtag	aatactgcta	3065
gtttcttaat	tttaattcac	atcacctgaa	aagtaaaaca	acaggctttg	ccaagtggat	3125
gcttttcagt	aacagtgaag	tggagtgaat	accaaagtgt	tgccctgggtg	gttcctatct	3185

32600PWO.ST25.txt

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cttcaggcaa acatgggtcag tattctgttaa agttcccctg gcctaaatga ttacttgctc 3245
tgggcaagtg gatatttatt aggctatttc aaagccacag cataagaatg tcagcctagc 3305
cacagagtct gagattctga gttcagccta gccacagagt ctaagattct gtatcctctg 3365
acattttgga aatgatacac tactggctta agtgatgact ctttcagatt ttcagtattt 3425
tatacaacta ctgccacatc cttatacttt attgcttttc tgtcttcttc aacctgggag 3485
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agcaggggta aaactaccac ctggcctagc ctaagtagga agtgaaaaga taattcacca 3665
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gagctgactt gtaaactatt cttgtaatag ctcattattt tgaaagattt atatatgatg 4085
aattctggat atatgaccaa taaaactgat gaagcaaaaa aaaaaaaaaa aaaaaaaaaa 4144

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<210> 45
 <211> 146
 <212> PRT
 <213> Homo sapiens

<400> 45

Met Thr Met Arg Ser Leu Leu Arg Thr Pro Phe Leu Cys Gly Leu Leu
 1 5 10 15

Trp Ala Phe Cys Ala Pro Gly Ala Arg Ala Glu Glu Pro Ala Ala Ser
 20 25 30

Phe Ser Gln Pro Gly Ser Met Gly Leu Asp Lys Asn Thr Val His Asp
 35 40 45

Gln Glu His Ile Met Glu His Leu Glu Gly Val Ile Asn Lys Pro Glu
 50 55 60

Ala Glu Met Ser Pro Gln Glu Leu Gln Leu His Tyr Phe Lys Met His
 65 70 75 80

Asp Tyr Asp Gly Asn Asn Leu Leu Asp Gly Leu Glu Leu Ser Thr Ala
 85 90 95

Ile Thr His Val His Lys Glu Glu Gly Ser Glu Gln Ala Pro Leu Met
 100 105 110

32600PWO.ST25.txt

Ser Glu Asp Glu Leu Ile Asn Ile Ile Asp Gly Val Leu Arg Asp Asp
 115 120 125

Asp Lys Asn Asn Asp Gly Tyr Ile Asp Tyr Ala Glu Phe Ala Lys Ser
 130 135 140

Leu Gln
 145

<210> 46
 <211> 1513
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (37)..(810)
 <223> SF10, cDNA: NM_029568, Protein: NP_083844

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 Met Lys Ala Leu Pro Ala
 1 5

ctg cca ctg atg ctg atg ctg ctc tcc atg cct ccc ccc tgc gcc ccg 102
 Leu Pro Leu Met Leu Met Leu Leu Ser Met Pro Pro Pro Cys Ala Pro
 10 15 20

caa gcc tct ggg atc cgg gga gat gct ctg gag aag tcc tgt ctt cag 150
 Gln Ala Ser Gly Ile Arg Gly Asp Ala Leu Glu Lys Ser Cys Leu Gln
 25 30 35

caa ccc ctg gac tgt gat gat atc tac gcc cag ggc tat cag gaa gac 198
 Gln Pro Leu Asp Cys Asp Asp Ile Tyr Ala Gln Gly Tyr Gln Glu Asp
 40 45 50

ggc gtg tat ctc atc tac ccc tat ggc ccc agt gtg ccg gtg ccc gtc 246
 Gly Val Tyr Leu Ile Tyr Pro Tyr Gly Pro Ser Val Pro Val Pro Val
 55 60 65 70

ttc tgc gac atg aca act gag ggc ggc aag tgg acg gtt ttc cag aaa 294
 Phe Cys Asp Met Thr Thr Glu Gly Gly Lys Trp Thr Val Phe Gln Lys
 75 80 85

aga ttc aac ggc tca gtg agt ttc ttc cgg ggc tgg agc gac tac aag 342
 Arg Phe Asn Gly Ser Val Ser Phe Phe Arg Gly Trp Ser Asp Tyr Lys
 90 95 100

ctg ggc ttt ggc cgt gct gac ggg gag tac tgg ctg ggc ctg cag aac 390
 Leu Gly Phe Gly Arg Ala Asp Gly Glu Tyr Trp Leu Gly Leu Gln Asn
 105 110 115

ctg cac ctc ctg aca ctg aag cag aag tat gag ctg cgc gtg gac ttg 438
 Leu His Leu Leu Thr Leu Lys Gln Lys Tyr Glu Leu Arg Val Asp Leu
 120 125 130

gaa gac ttt gag aac aac aca gcc tat gcc aag tac att gac ttc tcc 486
 Glu Asp Phe Glu Asn Asn Thr Ala Tyr Ala Lys Tyr Ile Asp Phe Ser
 135 140 145 150

atc tcc ccc aac gcc atc agt gct gag gag gat ggc tat acc ctc tac 534
 Ile Ser Pro Asn Ala Ile Ser Ala Glu Glu Asp Gly Tyr Thr Leu Tyr
 155 160 165

32600PWO.ST25.txt

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gtg gct ggc ttc gag gat ggc ggg gca ggt gac tca ctg tcc tac cac      582
Val Ala Gly Phe Glu Asp Gly Gly Ala Gly Asp Ser Leu Ser Tyr His
          170          175          180

agt ggc cag aag ttc tcc acc ttt gat cgg gac cag gac ctc ttc gtg      630
Ser Gly Gln Lys Phe Ser Thr Phe Asp Arg Asp Gln Asp Leu Phe Val
          185          190          195

cag aac tgt gca gcc ctc tcc tca gga gcc ttc tgg ttc cga agc tgc      678
Gln Asn Cys Ala Ala Leu Ser Ser Gly Ala Phe Trp Phe Arg Ser Cys
          200          205          210

cat ttc gcc aat ctc aac ggt ttc tac ctg ggt ggt tcc cat ctc tcc      726
His Phe Ala Asn Leu Asn Gly Phe Tyr Leu Gly Gly Ser His Leu Ser
          215          220          225          230

tat gcc aat ggc atc aat tgg gcc caa tgg aaa ggc ttc tat tac tcc      774
Tyr Ala Asn Gly Ile Asn Trp Ala Gln Trp Lys Gly Phe Tyr Tyr Ser
          235          240          245

ctc aag cgc acg gag atg aaa att cgt cgg gcc tga ggggctggcc      820
Leu Lys Arg Thr Glu Met Lys Ile Arg Arg Ala
          250          255

caagcaggcc ccattctttcc cctgaagtcc caaggggtcca tgttctccct ccacgcttta      880

cccacaattc ctgagcacca gccatgccct ggcaaatecc tgtcccacat acagccacgc      940

cctgatgcat tccacctgag gctaggctgt cagcagccct ccaggccttt ctgtggctga      1000

gccatcctag cctggatctg gctgaaatcc attaaaaact ccaagttgct tctaccctt      1060

cacgacagct gaaagccaga agctaccttc tagctgccag cttttgcacc ccacctcagc      1120

agtttcttta ctgcagagcc ttctgtttgg ggctaccctc gacagagtca tgcagcacct      1180

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agaatacttc ctaccttggc ctcatcactt tactccctac gtgagcatca tggagcccaa      1300

tcccatctgc cttcactcat cctcaaaaat tcaccaccaa aacaatactc accacggcta      1360

ctgctcaact ctgaagtcgt catggcaaag ataggcttgt tgacttggtc ccctacttgc      1420

cctagcgatc gtcatgagag gcagcaggga tcaatatgtg gggctggaag tgggtgggta      1480

gcagaggtct caataaactt caggatctga tgg      1513

```

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<210> 47
<211> 257
<212> PRT
<213> Mus musculus

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<400> 47
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Met Lys Ala Leu Pro Ala Leu Pro Leu Met Leu Met Leu Leu Ser Met
1          5          10          15

```

```

Pro Pro Pro Cys Ala Pro Gln Ala Ser Gly Ile Arg Gly Asp Ala Leu
          20          25          30

```

```

Glu Lys Ser Cys Leu Gln Gln Pro Leu Asp Cys Asp Asp Ile Tyr Ala
          35          40          45

```

32600PWO.ST25.txt

Gln Gly Tyr Gln Glu Asp Gly Val Tyr Leu Ile Tyr Pro Tyr Gly Pro
50 55 60

Ser Val Pro Val Pro Val Phe Cys Asp Met Thr Thr Glu Gly Gly Lys
65 70 75 80

Trp Thr Val Phe Gln Lys Arg Phe Asn Gly Ser Val Ser Phe Phe Arg
85 90 95

Gly Trp Ser Asp Tyr Lys Leu Gly Phe Gly Arg Ala Asp Gly Glu Tyr
100 105 110

Trp Leu Gly Leu Gln Asn Leu His Leu Leu Thr Leu Lys Gln Lys Tyr
115 120 125

Glu Leu Arg Val Asp Leu Glu Asp Phe Glu Asn Asn Thr Ala Tyr Ala
130 135 140

Lys Tyr Ile Asp Phe Ser Ile Ser Pro Asn Ala Ile Ser Ala Glu Glu
145 150 155 160

Asp Gly Tyr Thr Leu Tyr Val Ala Gly Phe Glu Asp Gly Gly Ala Gly
165 170 175

Asp Ser Leu Ser Tyr His Ser Gly Gln Lys Phe Ser Thr Phe Asp Arg
180 185 190

Asp Gln Asp Leu Phe Val Gln Asn Cys Ala Ala Leu Ser Ser Gly Ala
195 200 205

Phe Trp Phe Arg Ser Cys His Phe Ala Asn Leu Asn Gly Phe Tyr Leu
210 215 220

Gly Gly Ser His Leu Ser Tyr Ala Asn Gly Ile Asn Trp Ala Gln Trp
225 230 235 240

Lys Gly Phe Tyr Tyr Ser Leu Lys Arg Thr Glu Met Lys Ile Arg Arg
245 250 255

Ala

<210> 48
<211> 1830
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (26)..(793)
<223> SF10, cDNA: NM_002404, Protein: NP_002395

32600PWO.ST25.txt

<400> 48

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agccactctg agcagaactg acagc atg aag gca ctc ctg gcc ctg ccg ctg      52
                        Met Lys Ala Leu Leu Ala Leu Pro Leu
                        1                               5

ctg ctg ctt ctc tcc acg ccc ccg tgt gcc ccc cag gtc tcc ggg atc      100
Leu Leu Leu Leu Ser Thr Pro Pro Cys Ala Pro Gln Val Ser Gly Ile
10                               15                20        25

cga gga gat gct ctg gag agg ttt tgc ctt cag caa ccc ctg gac tgt      148
Arg Gly Asp Ala Leu Glu Arg Phe Cys Leu Gln Gln Pro Leu Asp Cys
                        30                               35        40

gac gac atc tat gcc cag ggc tac cag tca gac ggc gtg tac ctc atc      196
Asp Asp Ile Tyr Ala Gln Gly Tyr Gln Ser Asp Gly Val Tyr Leu Ile
                        45                               50        55

tac ccc tcg ggc ccc agt gtg cct gtg ccc gtc ttc tgt gac atg acc      244
Tyr Pro Ser Gly Pro Ser Val Pro Val Pro Val Phe Cys Asp Met Thr
                        60                               65        70

acc gag ggc ggg aag tgg acg gtt ttc cag aag aga ttc aat ggc tca      292
Thr Glu Gly Gly Lys Trp Thr Val Phe Gln Lys Arg Phe Asn Gly Ser
                        75                               80        85

gta agt ttc ttc cgc ggc tgg aat gac tac aag ctg ggc ttc ggc cgt      340
Val Ser Phe Phe Arg Gly Trp Asn Asp Tyr Lys Leu Gly Phe Gly Arg
90                               95        100       105

gct gat gga gag tac tgg ctg ggg ctg cag aac atg cac ctc ctg aca      388
Ala Asp Gly Glu Tyr Trp Leu Gly Leu Gln Asn Met His Leu Leu Thr
                        110                               115        120

ctg aag cag aag tat gag ctg cga gtg gac ttg gag gac ttt gag aac      436
Leu Lys Gln Lys Tyr Glu Leu Arg Val Asp Leu Glu Asp Phe Glu Asn
                        125                               130        135

aac acg gcc tat gcc aag tac gct gac ttc tcc atc tcc ccg aac gcg      484
Asn Thr Ala Tyr Ala Lys Tyr Ala Asp Phe Ser Ile Ser Pro Asn Ala
                        140                               145        150

gtc agc gca gag gag gat ggc tac acc ctc ttt gtg gca ggc ttt gag      532
Val Ser Ala Glu Glu Asp Gly Tyr Thr Leu Phe Val Ala Gly Phe Glu
155                               160        165

gat ggc ggg gca ggt gac tcc ctg tcc tac cac agt ggc cag aag ttc      580
Asp Gly Gly Ala Gly Asp Ser Leu Ser Tyr His Ser Gly Gln Lys Phe
170                               175        180       185

tct acc ttc gac cgg gac cag gac ctc ttt gtg cag aac tgc gca gct      628
Ser Thr Phe Asp Arg Asp Gln Asp Leu Phe Val Gln Asn Cys Ala Ala
                        190                               195        200

ctc tcc tca gga gcc ttc tgg ttc cgc agc tgc cac ttt gcc aac ctc      676
Leu Ser Ser Gly Ala Phe Trp Phe Arg Ser Cys His Phe Ala Asn Leu
205                               210        215

aat ggc ttc tac cta ggt ggc tcc cac ctc tct tat gcc aat ggc atc      724
Asn Gly Phe Tyr Leu Gly Gly Ser His Leu Ser Tyr Ala Asn Gly Ile
                        220                               225        230

aac tgg gcc cag tgg aag ggc ttc tac tac tcc ctc aaa cgc act gag      772
Asn Trp Ala Gln Trp Lys Gly Phe Tyr Tyr Ser Leu Lys Arg Thr Glu
235                               240        245

atg aaa atc cgc cgg gcc tga agggctggcc ccctcaggca cctttcctcc      823
Met Lys Ile Arg Arg Ala
250                               255

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32600PWO.ST25.txt

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cctggacacc catggtctcc atgagtgtct cctctgtctgc ccctgatgca tgctttctgct 883
gattccccgag caccaactcc ttacaagggg gccttgtggc tctcagccat gccacatccc 943
tgtcacacac ccagggcatc cattcctaag ccagacccgg ctcccctaca cctgaagtta 1003
cactgccagc agttccccag gcctcttccg agaggcacat ggttctagcc tggacctggc 1063
tggtgtccat gagaatgagt tgcttccacc ctgtcccaac agctgacagc caggagccac 1123
tctcccagct gcaggccttt gtggtccatc ttgtcctgct tctcactgt ggacctctgt 1183
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ctaggccaca gccagcact cctctgggct gctctcaaac catgtcccat cttcagcatc 1303
cctcccacca acttactccc ctgtggtgag taccgtggaa cccagccca cctcactatc 1363
atactcagct tcccctgatg gccatccca gccctgaag ctctatgcca agaacacagc 1423
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tcatacacac aaacatattt gtttatcccc caaatgtagg cacctggctc ctcttgctc 1663
ccctgctgat ggtgtcctac cccgaactcc aaaaattaca cctggagtca ggtgcagaag 1723
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ataataataa aaatataata ctgaaaagga aaaaaaaaaa aaaaaaa 1830

```

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<210> 49
<211> 255
<212> PRT
<213> Homo sapiens

```

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<400> 49
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Met Lys Ala Leu Leu Ala Leu Pro Leu Leu Leu Leu Ser Thr Pro
1          5          10          15
```

```
Pro Cys Ala Pro Gln Val Ser Gly Ile Arg Gly Asp Ala Leu Glu Arg
20          25          30
```

```
Phe Cys Leu Gln Gln Pro Leu Asp Cys Asp Asp Ile Tyr Ala Gln Gly
35          40          45
```

```
Tyr Gln Ser Asp Gly Val Tyr Leu Ile Tyr Pro Ser Gly Pro Ser Val
50          55          60
```

```
Pro Val Pro Val Phe Cys Asp Met Thr Thr Glu Gly Gly Lys Trp Thr
65          70          75          80
```

```
Val Phe Gln Lys Arg Phe Asn Gly Ser Val Ser Phe Phe Arg Gly Trp
85          90          95
```

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Asn Asp Tyr Lys Leu Gly Phe Gly Arg Ala Asp Gly Glu Tyr Trp Leu
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100

105

110

Gly Leu Gln Asn Met His Leu Leu Thr Leu Lys Gln Lys Tyr Glu Leu
 115 120 125

Arg Val Asp Leu Glu Asp Phe Glu Asn Asn Thr Ala Tyr Ala Lys Tyr
 130 135 140

Ala Asp Phe Ser Ile Ser Pro Asn Ala Val Ser Ala Glu Glu Asp Gly
 145 150 155 160

Tyr Thr Leu Phe Val Ala Gly Phe Glu Asp Gly Gly Ala Gly Asp Ser
 165 170 175

Leu Ser Tyr His Ser Gly Gln Lys Phe Ser Thr Phe Asp Arg Asp Gln
 180 185 190

Asp Leu Phe Val Gln Asn Cys Ala Ala Leu Ser Ser Gly Ala Phe Trp
 195 200 205

Phe Arg Ser Cys His Phe Ala Asn Leu Asn Gly Phe Tyr Leu Gly Gly
 210 215 220

Ser His Leu Ser Tyr Ala Asn Gly Ile Asn Trp Ala Gln Trp Lys Gly
 225 230 235 240

Phe Tyr Tyr Ser Leu Lys Arg Thr Glu Met Lys Ile Arg Arg Ala
 245 250 255

<210> 50
 <211> 749
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (93)..(515)
 <223> SF11, cDNA: NM_009976, Protein: NP_034106

<400> 50
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gttggagctt tatccctttg tcctagccaa cc atg gcc agc ccg ctg cgc tcc 113
 Met Ala Ser Pro Leu Arg Ser
 1 5

ttg ctg ttc ctg ctg gcc gtc ctg gcc gtg gcc tgg gcg gcg acc cca 161
 Leu Leu Phe Leu Leu Ala Val Leu Ala Val Ala Trp Ala Ala Thr Pro
 10 15 20

aaa caa ggc ccg cga atg ttg gga gcc ccg gag gag gca gat gcc aat 209
 Lys Gln Gly Pro Arg Met Leu Gly Ala Pro Glu Glu Ala Asp Ala Asn
 25 30 35

gag gaa ggc gtg cgg cga gcg ttg gac ttc gct gtg agc gag tac aac 257
 Glu Glu Gly Val Arg Arg Ala Leu Asp Phe Ala Val Ser Glu Tyr Asn
 40 45 50 55

32600PWO.ST25.txt

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aag ggc agc aac gat gcg tac cac agc cgc gcc ata cag gtg gtg aga      305
Lys Gly Ser Asn Asp Ala Tyr His Ser Arg Ala Ile Gln Val Val Arg
              60              65              70

gct cgt aag cag ctc gtg gct gga gtg aac tat ttt ttg gat gtg gag      353
Ala Arg Lys Gln Leu Val Ala Gly Val Asn Tyr Phe Leu Asp Val Glu
              75              80              85

atg ggc cga act aca tgt acc aag tcc cag aca aat ttg act gac tgt      401
Met Gly Arg Thr Thr Cys Thr Lys Ser Gln Thr Asn Leu Thr Asp Cys
              90              95              100

cct ttc cat gac cag ccc cat ctg atg agg aag gca ctc tgc tcc ttc      449
Pro Phe His Asp Gln Pro His Leu Met Arg Lys Ala Leu Cys Ser Phe
              105              110              115

cag atc tac agc gtg ccc tgg aaa ggc aca cac tcc ctg aca aaa ttc      497
Gln Ile Tyr Ser Val Pro Trp Lys Gly Thr His Ser Leu Thr Lys Phe
              120              125              130              135

agc tgc aaa aat gcc taa gggctgagtc tagaaggatc atgcagactg      545
Ser Cys Lys Asn Ala
              140

ttccttactt gtgtccttc cctatagtgt ttcattctgc agaagggtgc tccggctctg      605

gagggcaccg ccagtgtgtt tgcaccagga gacagtaaag gagctgctgc aggcaggttc      665

tgcacatctg aacagctgtc ccctggctcc actcttcttg cagtacctgc catgccttgc      725

tcaattaaaa aaaaaaaaaa ttcg      749

<210> 51
<211> 140
<212> PRT
<213> Mus musculus

<400> 51

Met Ala Ser Pro Leu Arg Ser Leu Leu Phe Leu Leu Ala Val Leu Ala
1              5              10              15

Val Ala Trp Ala Ala Thr Pro Lys Gln Gly Pro Arg Met Leu Gly Ala
20              25              30

Pro Glu Glu Ala Asp Ala Asn Glu Glu Gly Val Arg Arg Ala Leu Asp
35              40              45

Phe Ala Val Ser Glu Tyr Asn Lys Gly Ser Asn Asp Ala Tyr His Ser
50              55              60

Arg Ala Ile Gln Val Val Arg Ala Arg Lys Gln Leu Val Ala Gly Val
65              70              75              80

Asn Tyr Phe Leu Asp Val Glu Met Gly Arg Thr Thr Cys Thr Lys Ser
85              90              95

Gln Thr Asn Leu Thr Asp Cys Pro Phe His Asp Gln Pro His Leu Met
100              105              110

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32600PWO.ST25.txt

Arg Lys Ala Leu Cys Ser Phe Gln Ile Tyr Ser Val Pro Trp Lys Gly
 115 120 125

Thr His Ser Leu Thr Lys Phe Ser Cys Lys Asn Ala
 130 135 140

<210> 52
 <211> 818
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (76)..(516)
 <223> SF11, cDNA: NM_000099, Protein: NP_000090

<400> 52
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 gcgtcctagc cgacc atg gcc ggg ccc ctg cgc gcc ccg ctg ctc ctg ctg 111
 Met Ala Gly Pro Leu Arg Ala Pro Leu Leu Leu Leu
 1 5 10
 gcc atc ctg gcc gtg gcc ctg gcc gtg agc ccc gcg gcc ggc tcc agt 159
 Ala Ile Leu Ala Val Ala Leu Ala Val Ser Pro Ala Ala Gly Ser Ser
 15 20 25
 ccc ggc aag ccg ccg cgc ctg gtg gga ggc ccc atg gac gcc agc gtg 207
 Pro Gly Lys Pro Pro Arg Leu Val Gly Gly Pro Met Asp Ala Ser Val
 30 35 40
 gag gag gag ggt gtg cgg cgt gca ctg gac ttt gcc gtc ggc gag tac 255
 Glu Glu Glu Gly Val Arg Arg Ala Leu Asp Phe Ala Val Gly Glu Tyr
 45 50 55 60
 aac aaa gcc agc aac gac atg tac cac agc cgc gcg ctg cag gtg gtg 303
 Asn Lys Ala Ser Asn Asp Met Tyr His Ser Arg Ala Leu Gln Val Val
 65 70 75
 cgc gcc cgc aag cag atc gta gct ggg gtg aac tac ttc ttg gac gtg 351
 Arg Ala Arg Lys Gln Ile Val Ala Gly Val Asn Tyr Phe Leu Asp Val
 80 85 90
 gag ctg ggc cga acc acg tgt acc aag acc cag ccc aac ttg gac aac 399
 Glu Leu Gly Arg Thr Thr Cys Thr Lys Thr Gln Pro Asn Leu Asp Asn
 95 100 105
 tgc ccc ttc cat gac cag cca cat ctg aaa agg aaa gca ttc tgc tct 447
 Cys Pro Phe His Asp Gln Pro His Leu Lys Arg Lys Ala Phe Cys Ser
 110 115 120
 ttc cag atc tac gct gtg cct tgg cag ggc aca atg acc ttg tcg aaa 495
 Phe Gln Ile Tyr Ala Val Pro Trp Gln Gly Thr Met Thr Leu Ser Lys
 125 130 135 140
 tcc acc tgt cag gac gcc tag gggctctgtac cgggctggcc tgtgcctatc 546
 Ser Thr Cys Gln Asp Ala
 145
 acctcttatg cacacctccc accccctgta ttcccacccc tggactgggt gccctgcct 606
 tggggaagggt ctccccatgt gcctgcacca ggagacagac agagaaggca gcaggcggcc 666
 tttgttgctc agcaaggggc tctgccctcc ctcttctcctt cttgcttctc atagccccgg 726

32600PWO.ST25.txt

tgtgcggtgc atacaccccc acctcctgca ataaaatagt agcatcggca aaaaaaaaaa 786
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 818

<210> 53
 <211> 146
 <212> PRT
 <213> Homo sapiens

<400> 53

Met Ala Gly Pro Leu Arg Ala Pro Leu Leu Leu Leu Ala Ile Leu Ala
 1 5 10 15

Val Ala Leu Ala Val Ser Pro Ala Ala Gly Ser Ser Pro Gly Lys Pro
 20 25 30

Pro Arg Leu Val Gly Gly Pro Met Asp Ala Ser Val Glu Glu Glu Gly
 35 40 45

Val Arg Arg Ala Leu Asp Phe Ala Val Gly Glu Tyr Asn Lys Ala Ser
 50 55 60

Asn Asp Met Tyr His Ser Arg Ala Leu Gln Val Val Arg Ala Arg Lys
 65 70 75 80

Gln Ile Val Ala Gly Val Asn Tyr Phe Leu Asp Val Glu Leu Gly Arg
 85 90 95

Thr Thr Cys Thr Lys Thr Gln Pro Asn Leu Asp Asn Cys Pro Phe His
 100 105 110

Asp Gln Pro His Leu Lys Arg Lys Ala Phe Cys Ser Phe Gln Ile Tyr
 115 120 125

Ala Val Pro Trp Gln Gly Thr Met Thr Leu Ser Lys Ser Thr Cys Gln
 130 135 140

Asp Ala.
 145

<210> 54
 <211> 2709
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (124)..(2241)
 <223> SF12, cDNA: NM_010180, Protein: NP_034310

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32600PWO.ST25.txt

ccc atg gag cgc ccc gtg ccg tcg cgc ctc gtc ccg ctg ccg ctg ctg	168
Met Glu Arg Pro Val Pro Ser Arg Leu Val Pro Leu Pro Leu Leu	
1 5 10 15	
ctg ctc agc agc ctc tcg ctg ctg gca gcc cga gcg aat gca gac atc	216
Leu Leu Ser Ser Leu Ser Leu Leu Ala Ala Arg Ala Asn Ala Asp Ile	
20 25 30	
tcc atg gag gct tgc tgc acg gat cca aat cag atg gct aac cag cac	264
Ser Met Glu Ala Cys Cys Thr Asp Pro Asn Gln Met Ala Asn Gln His	
35 40 45	
agg gac tgc tcg ctg ccg tac acc tca gaa tcc aag gag tgc agg atg	312
Arg Asp Cys Ser Leu Pro Tyr Thr Ser Glu Ser Lys Glu Cys Arg Met	
50 55 60	
gtc cag gag caa tgt tgt cac aac caa ctg gaa gag ctg cac tgt gcc	360
Val Gln Glu Gln Cys Cys His Asn Gln Leu Glu Glu Leu His Cys Ala	
65 70 75	
acg ggc atc aac ctg gcc agc gag cca gaa ggc tgc gcc tcg ctc cac	408
Thr Gly Ile Asn Leu Ala Ser Glu Pro Glu Gly Cys Ala Ser Leu His	
80 85 90 95	
agc tac aac agt agc ctt gag acc atc ttc ata aag agg tgc tgc cac	456
Ser Tyr Asn Ser Ser Leu Glu Thr Ile Phe Ile Lys Arg Cys Cys His	
100 105 110	
tgt tgc atg ctg gga aag gca tcc ctg gcc cga gac cag acc tgt gaa	504
Cys Cys Met Leu Gly Lys Ala Ser Leu Ala Arg Asp Gln Thr Cys Glu	
115 120 125	
ccc att gtc atg ata agc tac cag tgt ggg ctg gtg ttc cgt gcc tgc	552
Pro Ile Val Met Ile Ser Tyr Gln Cys Gly Leu Val Phe Arg Ala Cys	
130 135 140	
tgt gtg aag gcc cgg gag aat tca gac ttt gtc caa ggc aac ggt gca	600
Cys Val Lys Ala Arg Glu Asn Ser Asp Phe Val Gln Gly Asn Gly Ala	
145 150 155	
gac ctt cag gac cca gct aag att cct gac gag gag gac caa gaa gac	648
Asp Leu Gln Asp Pro Ala Lys Ile Pro Asp Glu Glu Asp Gln Glu Asp	
160 165 170 175	
ccg tac ctg aat gac cgc tgt cga ggt ggc ggg ccc tgt aag cag cag	696
Pro Tyr Leu Asn Asp Arg Cys Arg Gly Gly Gly Pro Cys Lys Gln Gln	
180 185 190	
tgc cgt gac act ggg gac gag gtg atc tgc tct tgc ttt gtg ggc tac	744
Cys Arg Asp Thr Gly Asp Glu Val Ile Cys Ser Cys Phe Val Gly Tyr	
195 200 205	
cag ctg cag tcg gat ggt gtc tcc tgc gaa gat atc aat gaa tgc atc	792
Gln Leu Gln Ser Asp Gly Val Ser Cys Glu Asp Ile Asn Glu Cys Ile	
210 215 220	
aca ggc agc cat aac tgc cgg ctg gga gaa tcc tgc atc aat aca gtg	840
Thr Gly Ser His Asn Cys Arg Leu Gly Glu Ser Cys Ile Asn Thr Val	
225 230 235	
ggc tct ttc cgc tgc cag cgg gac agc agc tgt ggg act ggc tat gag	888
Gly Ser Phe Arg Cys Gln Arg Asp Ser Ser Cys Gly Thr Gly Tyr Glu	
240 245 250 255	
ctc aca gag gat aat aac tgc aaa gat att gac gaa tgt gag act ggt	936
Leu Thr Glu Asp Asn Asn Cys Lys Asp Ile Asp Glu Cys Glu Thr Gly	
260 265 270	

32600PWO.ST25.txt

att cat aac tgc ccc ccc gat ttt atc tgt cag aat act ctg gga tcc Ile His Asn Cys Pro Pro Asp Phe Ile Cys Gln Asn Thr Leu Gly Ser 275 280 285	984
ttc cgt tgc aga ccg aag ctg cag tgc aag agc ggc ttc ata cag gat Phe Arg Cys Arg Pro Lys Leu Gln Cys Lys Ser Gly Phe Ile Gln Asp 290 295 300	1032
gct cta ggc aac tgc att gat atc aat gag tgt tta agt atc agt gct Ala Leu Gly Asn Cys Ile Asp Ile Asn Glu Cys Leu Ser Ile Ser Ala 305 310 315	1080
cca tgc cct gtg ggg cag aca tgc atc aat aca gag ggc tcc tac aca Pro Cys Pro Val Gly Gln Thr Cys Ile Asn Thr Glu Gly Ser Tyr Thr 320 325 330 335	1128
tgc cag aag aat gtg ccc aac tgt ggc cgt ggt tat cat ctc aat gaa Cys Gln Lys Asn Val Pro Asn Cys Gly Arg Gly Tyr His Leu Asn Glu 340 345 350	1176
gag ggg acc cgc tgt gtt gat gtg gat gag tgc gcc cca cca gcg gag Glu Gly Thr Arg Cys Val Asp Val Asp Glu Cys Ala Pro Pro Ala Glu 355 360 365	1224
ccc tgt ggg aag gga cac cac tgc ctg aac tcc ccc ggc agc ttc cgc Pro Cys Gly Lys Gly His His Cys Leu Asn Ser Pro Gly Ser Phe Arg 370 375 380	1272
tgc gag tgc aag gct ggc ttc tat ttt gat ggc atc agc agg acc tgc Cys Glu Cys Lys Ala Gly Phe Tyr Phe Asp Gly Ile Ser Arg Thr Cys 385 390 395	1320
gtg gat atc aac gag tgc cag cgc tat ccc ggg cgc ctg tgt ggc cac Val Asp Ile Asn Glu Cys Gln Arg Tyr Pro Gly Arg Leu Cys Gly His 400 405 410 415	1368
aag tgt gag aac acg cca ggc tcc ttc cac tgc agc tgc tcc gcc ggc Lys Cys Glu Asn Thr Pro Gly Ser Phe His Cys Ser Cys Ser Ala Gly 420 425 430	1416
ttc cgg ctg tct gtg gac ggc cgg tct tgt gaa gat gtg aac gag tgt Phe Arg Leu Ser Val Asp Gly Arg Ser Cys Glu Asp Val Asn Glu Cys 435 440 445	1464
ctc aac agc cct tgc agc cag gag tgt gct aat gtc tat ggc tcc tac Leu Asn Ser Pro Cys Ser Gln Glu Cys Ala Asn Val Tyr Gly Ser Tyr 450 455 460	1512
cag tgc tat tgc cga cga ggt tac cag ctc agt gac gtg gat ggg gtc Gln Cys Tyr Cys Arg Arg Gly Tyr Gln Leu Ser Asp Val Asp Gly Val 465 470 475	1560
acc tgc gaa gat att gat gag tgt gcc ctg ccc act gga ggt cac atc Thr Cys Glu Asp Ile Asp Glu Cys Ala Leu Pro Thr Gly Gly His Ile 480 485 490 495	1608
tgc tcc tac cgc tgc atc aac atc ccc gga agc ttc cag tgc agc tgc Cys Ser Tyr Arg Cys Ile Asn Ile Pro Gly Ser Phe Gln Cys Ser Cys 500 505 510	1656
ccc tca tct ggc tac agg cta gct ccc aat ggc cgc aac tgc caa gac Pro Ser Ser Gly Tyr Arg Leu Ala Pro Asn Gly Arg Asn Cys Gln Asp 515 520 525	1704
att gat gag tgt gtg acc ggc atc cat aac tgt tcc atc aat gag act Ile Asp Glu Cys Val Thr Gly Ile His Asn Cys Ser Ile Asn Glu Thr 530 535 540	1752

32600PWO.ST25.txt

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gag aac tat cgc cgc tcc gca gac acc ttc cgc caa gag aaa aca gac Glu Asn Tyr Arg Arg Ser Ala Asp Thr Phe Arg Gln Glu Lys Thr Asp 560 565 570 575	1848
acc gtc cgc tgc atc aag tct tgc cgt ccc aac gat gag gcc tgc gtg Thr Val Arg Cys Ile Lys Ser Cys Arg Pro Asn Asp Glu Ala Cys Val 580 585 590	1896
cgg gac cct gta cat acc gtc tcc cac acc gtc atc tcg ctg ccc acc Arg Asp Pro Val His Thr Val Ser His Thr Val Ile Ser Leu Pro Thr 595 600 605	1944
ttt cga gag ttc acc cgt cct gag gag atc atc ttt ctg agg gct gtc Phe Arg Glu Phe Thr Arg Pro Glu Glu Ile Ile Phe Leu Arg Ala Val 610 615 620	1992
aca ccg ctg tac ccc gcc aac cag gcc gac atc atc ttc gac atc aca Thr Pro Leu Tyr Pro Ala Asn Gln Ala Asp Ile Ile Phe Asp Ile Thr 625 630 635	2040
gaa ggg aac ctt cga gac tcc ttt gat atc atc aag cgc tat gag gac Glu Gly Asn Leu Arg Asp Ser Phe Asp Ile Ile Lys Arg Tyr Glu Asp 640 645 650 655	2088
ggc atg act gtg ggt gtc gtg cgc caa gtg cgg ccc atc gtg ggc ccg Gly Met Thr Val Gly Val Val Arg Gln Val Arg Pro Ile Val Gly Pro 660 665 670	2136
ttt tac gct gtc ctg aag ctg gag atg aac tac gtg ttg gga ggc gta Phe Tyr Ala Val Leu Lys Leu Glu Met Asn Tyr Val Leu Gly Gly Val 675 680 685	2184
gtt tcc cac cgg aac gtc gtc aat gta cac atc ttc gtc tcc gag tac Val Ser His Arg Asn Val Val Asn Val His Ile Phe Val Ser Glu Tyr 690 695 700	2232
tgg ttc tga gggccgggtt gcggctcagc caggagtgtg ccacgccctt Trp Phe 705	2281
gctgccagtg acagccaggt gcctgtctct acccctcggg cctcccttga tgtttcatat	2341
tggtttgtat ggccacgtgc attaggctga gccgaatcac ttaagtccag ctggtgtact	2401
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ccaattgaag gagttttcaa agcagactcc acccgaaagc cgaggcagcc agttctcact	2581
gagtctgcat gaggattggc attttggtac tttttttttt ttaaccaact gggctctttg	2641
tgtttcaagt tgatggctgc tgtagagtgg cgcataaata aatgtacaat aaattctccc	2701
cagaaaaa	2709

<210> 55
 <211> 705
 <212> PRT
 <213> Mus musculus

<400> 55

32600PWO.ST25.txt

Met Glu Arg Pro Val Pro Ser Arg Leu Val Pro Leu Pro Leu Leu Leu
1 5 10 15

Leu Ser Ser Leu Ser Leu Leu Ala Ala Arg Ala Asn Ala Asp Ile Ser
20 25 30

Met Glu Ala Cys Cys Thr Asp Pro Asn Gln Met Ala Asn Gln His Arg
35 40 45

Asp Cys Ser Leu Pro Tyr Thr Ser Glu Ser Lys Glu Cys Arg Met Val
50 55 60

Gln Glu Gln Cys Cys His Asn Gln Leu Glu Glu Leu His Cys Ala Thr
65 70 75 80

Gly Ile Asn Leu Ala Ser Glu Pro Glu Gly Cys Ala Ser Leu His Ser
85 90 95

Tyr Asn Ser Ser Leu Glu Thr Ile Phe Ile Lys Arg Cys Cys His Cys
100 105 110

Cys Met Leu Gly Lys Ala Ser Leu Ala Arg Asp Gln Thr Cys Glu Pro
115 120 125

Ile Val Met Ile Ser Tyr Gln Cys Gly Leu Val Phe Arg Ala Cys Cys
130 135 140

Val Lys Ala Arg Glu Asn Ser Asp Phe Val Gln Gly Asn Gly Ala Asp
145 150 155 160

Leu Gln Asp Pro Ala Lys Ile Pro Asp Glu Glu Asp Gln Glu Asp Pro
165 170 175

Tyr Leu Asn Asp Arg Cys Arg Gly Gly Gly Pro Cys Lys Gln Gln Cys
180 185 190

Arg Asp Thr Gly Asp Glu Val Ile Cys Ser Cys Phe Val Gly Tyr Gln
195 200 205

Leu Gln Ser Asp Gly Val Ser Cys Glu Asp Ile Asn Glu Cys Ile Thr
210 215 220

Gly Ser His Asn Cys Arg Leu Gly Glu Ser Cys Ile Asn Thr Val Gly
225 230 235 240

Ser Phe Arg Cys Gln Arg Asp Ser Ser Cys Gly Thr Gly Tyr Glu Leu
245 250 255

Thr Glu Asp Asn Asn Cys Lys Asp Ile Asp Glu Cys Glu Thr Gly Ile
260 265 270

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His Asn Cys Pro Pro Asp Phe Ile Cys Gln Asn Thr Leu Gly Ser Phe
 275 280 285
 Arg Cys Arg Pro Lys Leu Gln Cys Lys Ser Gly Phe Ile Gln Asp Ala
 290 295 300
 Leu Gly Asn Cys Ile Asp Ile Asn Glu Cys Leu Ser Ile Ser Ala Pro
 305 310 315 320
 Cys Pro Val Gly Gln Thr Cys Ile Asn Thr Glu Gly Ser Tyr Thr Cys
 325 330 335
 Gln Lys Asn Val Pro Asn Cys Gly Arg Gly Tyr His Leu Asn Glu Glu
 340 345 350
 Gly Thr Arg Cys Val Asp Val Asp Glu Cys Ala Pro Pro Ala Glu Pro
 355 360 365
 Cys Gly Lys Gly His His Cys Leu Asn Ser Pro Gly Ser Phe Arg Cys
 370 375 380
 Glu Cys Lys Ala Gly Phe Tyr Phe Asp Gly Ile Ser Arg Thr Cys Val
 385 390 395 400
 Asp Ile Asn Glu Cys Gln Arg Tyr Pro Gly Arg Leu Cys Gly His Lys
 405 410 415
 Cys Glu Asn Thr Pro Gly Ser Phe His Cys Ser Cys Ser Ala Gly Phe
 420 425 430
 Arg Leu Ser Val Asp Gly Arg Ser Cys Glu Asp Val Asn Glu Cys Leu
 435 440 445
 Asn Ser Pro Cys Ser Gln Glu Cys Ala Asn Val Tyr Gly Ser Tyr Gln
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 Cys Tyr Cys Arg Arg Gly Tyr Gln Leu Ser Asp Val Asp Gly Val Thr
 465 470 475 480
 Cys Glu Asp Ile Asp Glu Cys Ala Leu Pro Thr Gly Gly His Ile Cys
 485 490 495
 Ser Tyr Arg Cys Ile Asn Ile Pro Gly Ser Phe Gln Cys Ser Cys Pro
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 Ser Ser Gly Tyr Arg Leu Ala Pro Asn Gly Arg Asn Cys Gln Asp Ile
 515 520 525
 Asp Glu Cys Val Thr Gly Ile His Asn Cys Ser Ile Asn Glu Thr Cys
 530 535 540

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Phe Asn Ile Gln Gly Ser Phe Arg Cys Leu Ser Phe Glu Cys Pro Glu
545 550 555 560

Asn Tyr Arg Arg Ser Ala Asp Thr Phe Arg Gln Glu Lys Thr Asp Thr
565 570 575

Val Arg Cys Ile Lys Ser Cys Arg Pro Asn Asp Glu Ala Cys Val Arg
580 585 590

Asp Pro Val His Thr Val Ser His Thr Val Ile Ser Leu Pro Thr Phe
595 600 605

Arg Glu Phe Thr Arg Pro Glu Glu Ile Ile Phe Leu Arg Ala Val Thr
610 615 620

Pro Leu Tyr Pro Ala Asn Gln Ala Asp Ile Ile Phe Asp Ile Thr Glu
625 630 635 640

Gly Asn Leu Arg Asp Ser Phe Asp Ile Ile Lys Arg Tyr Glu Asp Gly
645 650 655

Met Thr Val Gly Val Val Arg Gln Val Arg Pro Ile Val Gly Pro Phe
660 665 670

Tyr Ala Val Leu Lys Leu Glu Met Asn Tyr Val Leu Gly Gly Val Val
675 680 685

Ser His Arg Asn Val Val Asn Val His Ile Phe Val Ser Glu Tyr Trp
690 695 700

Phe
705

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<223> SF12, cDNA: NM_006486, Protein: NP_006477

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ccgcccaccg cccgtcgccc gccgccc atg gag cgc gcc gcg ccg tcg cgc cgg 174
Met Glu Arg Ala Ala Pro Ser Arg Arg
1 5
gtc ccg ctt ccg ctg ctg ctg ctc ggc ggc ctt gcg ctg ctg gcg gcc 222
Val Pro Leu Pro Leu Leu Leu Leu Gly Gly Leu Ala Leu Leu Ala Ala
10 15 20 25

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gga	gtg	gac	gcg	gat	gtc	ctc	ctg	gag	gcc	tgc	tgt	gcg	gac	gga	cac	270
Gly	Val	Asp	Ala	Asp	Val	Leu	Leu	Glu	Ala	Cys	Cys	Ala	Asp	Gly	His	
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cgg	atg	gcc	act	cat	cag	aag	gac	tgc	tgc	ctg	cca	tat	gct	acg	gaa	318
Arg	Met	Ala	Thr	His	Gln	Lys	Asp	Cys	Ser	Leu	Pro	Tyr	Ala	Thr	Glu	
			45					50					55			
tcc	aaa	gaa	tgc	agg	atg	gtg	cag	gag	cag	tgc	tgc	cac	agc	cag	ctg	366
Ser	Lys	Glu	Cys	Arg	Met	Val	Gln	Glu	Gln	Cys	Cys	His	Ser	Gln	Leu	
		60					65					70				
gag	gag	ctg	cac	tgt	gcc	acg	ggc	atc	agc	ctg	gcc	aac	gag	cag	gac	414
Glu	Glu	Leu	His	Cys	Ala	Thr	Gly	Ile	Ser	Leu	Ala	Asn	Glu	Gln	Asp	
	75					80					85					
cgc	tgt	gcc	acg	ccc	cac	ggc	gac	aac	gcc	agc	ctg	gag	gcc	aca	ttt	462
Arg	Cys	Ala	Thr	Pro	His	Gly	Asp	Asn	Ala	Ser	Leu	Glu	Ala	Thr	Phe	
90					95					100					105	
gtg	aag	agg	tgc	tgc	cat	tgc	tgt	ctg	ctg	ggg	agg	gcg	gcc	cag	gcc	510
Val	Lys	Arg	Cys	Cys	His	Cys	Cys	Leu	Leu	Gly	Arg	Ala	Ala	Gln	Ala	
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cag	ggc	cag	agc	tgc	gag	tac	agc	ctc	atg	gtt	ggc	tac	cag	tgt	gga	558
Gln	Gly	Gln	Ser	Cys	Glu	Tyr	Ser	Leu	Met	Val	Gly	Tyr	Gln	Cys	Gly	
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cag	gtc	ttc	cgg	gca	tgc	tgt	gtc	aag	agc	cag	gag	acc	gga	gat	ttg	606
Gln	Val	Phe	Arg	Ala	Cys	Cys	Val	Lys	Ser	Gln	Glu	Thr	Gly	Asp	Leu	
		140					145					150				
gat	gtc	ggg	ggc	ctc	caa	gaa	acg	gat	aag	atc	att	gag	gtt	gag	gag	654
Asp	Val	Gly	Gly	Leu	Gln	Glu	Thr	Asp	Lys	Ile	Ile	Glu	Val	Glu	Glu	
	155					160					165					
gaa	caa	gag	gac	cca	tat	ctg	aat	gac	cgc	tgc	cga	gga	ggc	ggg	ccc	702
Glu	Gln	Glu	Asp	Pro	Tyr	Leu	Asn	Asp	Arg	Cys	Arg	Gly	Gly	Gly	Pro	
170					175					180					185	
tgc	aag	cag	cag	tgc	cga	gac	acg	ggc	gac	gag	gtg	gtc	tgc	tcc	tgc	750
Cys	Lys	Gln	Gln	Cys	Arg	Asp	Thr	Gly	Asp	Glu	Val	Val	Cys	Ser	Cys	
				190					195					200		
ttc	gtg	ggc	tac	cag	ctg	ctg	tct	gat	ggc	gtc	tcc	tgt	gaa	gat	gtc	798
Phe	Val	Gly	Tyr	Gln	Leu	Leu	Ser	Asp	Gly	Val	Ser	Cys	Glu	Asp	Val	
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aat	gaa	tgc	atc	acg	ggc	agc	cac	agc	tgc	cgg	ctt	gga	gaa	tcc	tgc	846
Asn	Glu	Cys	Ile	Thr	Gly	Ser	His	Ser	Cys	Arg	Leu	Gly	Glu	Ser	Cys	
		220					225					230				
atc	aac	aca	gtg	ggc	tct	ttc	cgc	tgc	cag	cgg	gac	agc	agc	tgc	ggg	894
Ile	Asn	Thr	Val	Gly	Ser	Phe	Arg	Cys	Gln	Arg	Asp	Ser	Ser	Cys	Gly	
	235					240					245					
act	ggc	tat	gag	ctc	aca	gag	gac	aat	agc	tgc	aaa	gat	att	gac	gag	942
Thr	Gly	Tyr	Glu	Leu	Thr	Glu	Asp	Asn	Ser	Cys	Lys	Asp	Ile	Asp	Glu	
250					255					260					265	
tgt	gag	agt	ggc	att	cat	aac	tgc	ctc	ccc	gat	ttt	atc	tgt	cag	aat	990
Cys	Glu	Ser	Gly	Ile	His	Asn	Cys	Leu	Pro	Asp	Phe	Ile	Cys	Gln	Asn	
				270					275					280		
act	ctg	gga	tcc	ttc	cgc	tgc	cga	ccc	aag	cta	cag	tgc	aag	agt	ggc	1038
Thr	Leu	Gly	Ser	Phe	Arg	Cys	Arg	Pro	Lys	Leu	Gln	Cys	Lys	Ser	Gly	
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ttt ata caa gat gct cta ggc aac tgt att gat atc aat gag tgt ttg	1086
Phe Ile Gln Asp Ala Leu Gly Asn Cys Ile Asp Ile Asn Glu Cys Leu	
300 305 310	
agt atc agt gcc ccg tgc cct atc ggg cat aca tgc atc aac aca gag	1134
Ser Ile Ser Ala Pro Cys Pro Ile Gly His Thr Cys Ile Asn Thr Glu	
315 320 325	
ggc tcc tac acg tgc cag aag aac gtg ccc aac tgt ggc cgt ggc tac	1182
Gly Ser Tyr Thr Cys Gln Lys Asn Val Pro Asn Cys Gly Arg Gly Tyr	
330 335 340 345	
cat ctc aac gag gag gga acg cgc tgt gtt gat gtg gac gag tgc gcg	1230
His Leu Asn Glu Glu Gly Thr Arg Cys Val Asp Val Asp Glu Cys Ala	
350 355 360	
cca cct gct gag ccc tgt ggg aag gga cat cgc tgc gtg aac tct ccc	1278
Pro Pro Ala Glu Pro Cys Gly Lys Gly His Arg Cys Val Asn Ser Pro	
365 370 375	
ggc agt ttc cgc tgc gaa tgc aag acg ggt tac tat ttt gac ggc atc	1326
Gly Ser Phe Arg Cys Glu Cys Lys Thr Gly Tyr Tyr Phe Asp Gly Ile	
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agc agg atg tgt gtc gat gtc aac gag tgc cag cgc tac ccc ggg cgc	1374
Ser Arg Met Cys Val Asp Val Asn Glu Cys Gln Arg Tyr Pro Gly Arg	
395 400 405	
ctg tgt ggc cac aag tgc gag aac acg ctg ggc tcc tac ctc tgc agc	1422
Leu Cys Gly His Lys Cys Glu Asn Thr Leu Gly Ser Tyr Leu Cys Ser	
410 415 420 425	
tgt tcc gtg ggc ttc cgg ctc tct gtg gat ggc agg tca tgt gaa gac	1470
Cys Ser Val Gly Phe Arg Leu Ser Val Asp Gly Arg Ser Cys Glu Asp	
430 435 440	
atc aat gag tgc agc agc agc ccc tgt agc cag gag tgt gcc aac gtc	1518
Ile Asn Glu Cys Ser Ser Ser Pro Cys Ser Gln Glu Cys Ala Asn Val	
445 450 455	
tac ggc tcc tac cag tgt tac tgc cgg cga ggc tac cag ctc agc gat	1566
Tyr Gly Ser Tyr Gln Cys Tyr Cys Arg Arg Gly Tyr Gln Leu Ser Asp	
460 465 470	
gtg gat gga gtc acc tgt gaa gac atc gac gag tgc gcc ctg ccc acc	1614
Val Asp Gly Val Thr Cys Glu Asp Ile Asp Glu Cys Ala Leu Pro Thr	
475 480 485	
ggg ggc cac atc tgc tcc tac cgc tgc atc aac atc cct gga agc ttc	1662
Gly Gly His Ile Cys Ser Tyr Arg Cys Ile Asn Ile Pro Gly Ser Phe	
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cag tgc agc tgc ccc tgc tct ggc tac agg ctg gcc ccc aat ggc cgc	1710
Gln Cys Ser Cys Pro Ser Ser Gly Tyr Arg Leu Ala Pro Asn Gly Arg	
510 515 520	
aac tgc caa gac att gat gag tgt gtg act ggc atc cac aac tgc tcc	1758
Asn Cys Gln Asp Ile Asp Glu Cys Val Thr Gly Ile His Asn Cys Ser	
525 530 535	
atc aac gag acc tgc ttc aac atc cag ggc ggc ttc cgc tgc ctg gcc	1806
Ile Asn Glu Thr Cys Phe Asn Ile Gln Gly Gly Phe Arg Cys Leu Ala	
540 545 550	
ttc gag tgc cct gag aac tac cgc cgc tcc gca gcc acg ctc cag cag	1854
Phe Glu Cys Pro Glu Asn Tyr Arg Arg Ser Ala Ala Thr Leu Gln Gln	
555 560 565	

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gag aag aca gac acg gtc cgc tgc atc aag tcc tgc cgc ccc aac gat      1902
Glu Lys Thr Asp Thr Val Arg Cys Ile Lys Ser Cys Arg Pro Asn Asp
570                               575                               580                               585

gtc aca tgc gtg ttc gac ccc gtg cac acc atc tcc cac acc gtc atc      1950
Val Thr Cys Val Phe Asp Pro Val His Thr Ile Ser His Thr Val Ile
                               590                               595                               600

tcg ctg cct acc ttc cgc gag ttc acc cgc cct gaa gag atc atc ttc      1998
Ser Leu Pro Thr Phe Arg Glu Phe Thr Arg Pro Glu Glu Ile Ile Phe
                               605                               610                               615

ctc cgg gcc atc acg cca ccg cat cct gcc agc cag gct aac atc atc      2046
Leu Arg Ala Ile Thr Pro Pro His Pro Ala Ser Gln Ala Asn Ile Ile
                               620                               625                               630

ttc gac atc acg gaa ggg aac ctg cgg gac tct ttt gac atc atc aag      2094
Phe Asp Ile Thr Glu Gly Asn Leu Arg Asp Ser Phe Asp Ile Ile Lys
635                               640                               645

cgt tac atg gac ggc atg acc gtg ggt gtc gtg cgc cag gtg cgg ccc      2142
Arg Tyr Met Asp Gly Met Thr Val Gly Val Val Arg Gln Val Arg Pro
650                               655                               660                               665

atc gtg ggc cca ttt cat gcc gtc ctg aag ctg gag atg aac tat gtg      2190
Ile Val Gly Pro Phe His Ala Val Leu Lys Leu Glu Met Asn Tyr Val
                               670                               675                               680

gtc ggg ggc gtg gtc tcc cac cga aat gtt gtc aac gtc cac atc ttc      2238
Val Gly Gly Val Val Ser His Arg Asn Val Val Asn Val His Ile Phe
685                               690                               695

gtc tct gag tac tgg ttc tga gggctggtct gccgcacagc cgcaggtgca      2289
Val Ser Glu Tyr Trp Phe
700

cctccaggcc aaatcattgc tgccagtgc tgtggtctgt acttgtttat accctcagac      2349

ttttttaatg ttaggtatgt gtagcattag gccaacatgt attaagctga gccagatgaa      2409

taagtccatc tgatgtatgt tcggtgttta aaaaatgagc ccagttgctc aactgtttgg      2469

ttgaaaacct tgctcatttt ttaatgcgaa ggctaagtgt caccctctct ctctgcctct      2529

ggctgggcct tgctaagggc caaggaaaga aagacatttt ttagggggca gccagtccaa      2589

atgccaaaag aagaccagtt cttgccctga ttgtatgaaa tttgacattt tggcactttt      2649

tttttttttt tggccaatca gattttctat gttctaagga catggctgct gtagaatagc      2709

acagacgtgg atgataaatt atccccagaa gcagcatgac agaatgcctc ggggagcact      2769

tggaagggaa attgcagttc tgttgaaata gaggaaaatc ccttggtaaa gacacagcct      2829

gttaggctcg tgtgggcctc cagtatgttc accaggggaa tggctgggat ttctcggcac      2889

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<211> 703
<212> PRT
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Leu Gly Gly Leu Ala Leu Leu Ala Ala Gly Val Asp Ala Asp Val Leu
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Leu Glu Ala Cys Cys Ala Asp Gly His Arg Met Ala Thr His Gln Lys
    35              40              45

Asp Cys Ser Leu Pro Tyr Ala Thr Glu Ser Lys Glu Cys Arg Met Val
    50              55              60

Gln Glu Gln Cys Cys His Ser Gln Leu Glu Glu Leu His Cys Ala Thr
    65              70              75              80

Gly Ile Ser Leu Ala Asn Glu Gln Asp Arg Cys Ala Thr Pro His Gly
    85              90              95

Asp Asn Ala Ser Leu Glu Ala Thr Phe Val Lys Arg Cys Cys His Cys
   100              105              110

Cys Leu Leu Gly Arg Ala Ala Gln Ala Gln Gly Gln Ser Cys Glu Tyr
   115              120              125

Ser Leu Met Val Gly Tyr Gln Cys Gly Gln Val Phe Arg Ala Cys Cys
   130              135              140

Val Lys Ser Gln Glu Thr Gly Asp Leu Asp Val Gly Gly Leu Gln Glu
   145              150              155              160

Thr Asp Lys Ile Ile Glu Val Glu Glu Glu Gln Glu Asp Pro Tyr Leu
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Asn Asp Arg Cys Arg Gly Gly Gly Pro Cys Lys Gln Gln Cys Arg Asp
   180              185              190

Thr Gly Asp Glu Val Val Cys Ser Cys Phe Val Gly Tyr Gln Leu Leu
   195              200              205

Ser Asp Gly Val Ser Cys Glu Asp Val Asn Glu Cys Ile Thr Gly Ser
   210              215              220

His Ser Cys Arg Leu Gly Glu Ser Cys Ile Asn Thr Val Gly Ser Phe
   225              230              235              240

Arg Cys Gln Arg Asp Ser Ser Cys Gly Thr Gly Tyr Glu Leu Thr Glu
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Asp Asn Ser Cys Lys Asp Ile Asp Glu Cys Glu Ser Gly Ile His Asn
   260              265              270

Cys Leu Pro Asp Phe Ile Cys Gln Asn Thr Leu Gly Ser Phe Arg Cys

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275

280

285

Arg Pro Lys Leu Gln Cys Lys Ser Gly Phe Ile Gln Asp Ala Leu Gly
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 305 310 315 320
 Ile Gly His Thr Cys Ile Asn Thr Glu Gly Ser Tyr Thr Cys Gln Lys
 325 330 335
 Asn Val Pro Asn Cys Gly Arg Gly Tyr His Leu Asn Glu Glu Gly Thr
 340 345 350
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 355 360 365
 Lys Gly His Arg Cys Val Asn Ser Pro Gly Ser Phe Arg Cys Glu Cys
 370 375 380
 Lys Thr Gly Tyr Tyr Phe Asp Gly Ile Ser Arg Met Cys Val Asp Val
 385 390 395 400
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 405 410 415
 Asn Thr Leu Gly Ser Tyr Leu Cys Ser Cys Ser Val Gly Phe Arg Leu
 420 425 430
 Ser Val Asp Gly Arg Ser Cys Glu Asp Ile Asn Glu Cys Ser Ser Ser
 435 440 445
 Pro Cys Ser Gln Glu Cys Ala Asn Val Tyr Gly Ser Tyr Gln Cys Tyr
 450 455 460
 Cys Arg Arg Gly Tyr Gln Leu Ser Asp Val Asp Gly Val Thr Cys Glu
 465 470 475 480
 Asp Ile Asp Glu Cys Ala Leu Pro Thr Gly Gly His Ile Cys Ser Tyr
 485 490 495
 Arg Cys Ile Asn Ile Pro Gly Ser Phe Gln Cys Ser Cys Pro Ser Ser
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 Gly Tyr Arg Leu Ala Pro Asn Gly Arg Asn Cys Gln Asp Ile Asp Glu
 515 520 525
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 Ile Gln Gly Gly Phe Arg Cys Leu Ala Phe Glu Cys Pro Glu Asn Tyr

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gtccggggctg	cccgaccgct	cttgctgctg	ccggtgg	atg	ctg	cgc	ctc	tcg	gag								115
					Met	Leu	Arg	Leu	Ser	Glu							
				1						5							
cgc	aat	atg	aag	gtg	ctc	ttc	gcc	gcc	gcc	ctc	atc	gtg	ggc	tcc	gtc	163	
Arg	Asn	Met	Lys	Val	Leu	Phe	Ala	Ala	Ala	Leu	Ile	Val	Gly	Ser	Val		
			10				15				20						
gtc	ttc	ctt	ttg	ctg	ccc	gga	ccc	tcc	gtg	gcc	aac	gat	aag	aag	aag	211	
Val	Phe	Leu	Leu	Pro	Gly	Pro	Ser	Val	Ala	Asn	Asp	Lys	Lys	Lys			
			25				30				35						
gga	cct	aaa	gtc	aca	gtc	aag	gta	tac	ttt	gat	tta	caa	att	gga	gat	259	
Gly	Pro	Lys	Val	Thr	Val	Lys	Val	Tyr	Phe	Asp	Leu	Gln	Ile	Gly	Asp		
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55 60 65 70

aaa aca gtg gat aat ttt gta gcc tta gct aca gga gag aaa gga ttt 355
Lys Thr Val Asp Asn Phe Val Ala Leu Ala Thr Gly Glu Lys Gly Phe
75 80 85

ggc tac aaa aac agc aag ttc cat cgt gtc atc aag gac ttc atg atc 403
Gly Tyr Lys Asn Ser Lys Phe His Arg Val Ile Lys Asp Phe Met Ile
90 95 100

cag ggt gga gac ttc acc agg gga gat ggc aca gga gga aag agc atc 451
Gln Gly Gly Asp Phe Thr Arg Gly Asp Gly Thr Gly Gly Lys Ser Ile
105 110 115

tat ggt gag cgc ttc cca gat gag aac ttc aag ctg aag cac tac ggg 499
Tyr Gly Glu Arg Phe Pro Asp Gly Asn Phe Lys Leu Lys His Tyr Gly
120 125 130

cct ggc tgg gtg agc atg gcc aat gca ggc aaa gac acc aat ggc tca 547
Pro Gly Trp Val Ser Met Ala Asn Ala Gly Lys Asp Thr Asn Gly Ser
135 140 145 150

cag ttc ttc ata acc aca gtc aag acc tcc tgg ctg gat ggc aag cat 595
Gln Phe Phe Ile Thr Thr Val Lys Thr Ser Trp Leu Asp Gly Lys His
155 160 165

gtg gtt ttc ggc aaa gtt cta gag ggc atg gat gtg gta cgg aag gtg 643
Val Val Phe Gly Lys Val Leu Glu Gly Met Asp Val Val Arg Lys Val
170 175 180

gag agc acc aag aca gac agc cgg gac aag cca ctg aag gat gtc atc 691
Glu Ser Thr Lys Thr Asp Ser Arg Asp Lys Pro Leu Lys Asp Val Ile
185 190 195

att gtc gac tcc ggc aag atc gaa gtg gag aaa ccc ttc gcc att gcc 739
Ile Val Asp Ser Gly Lys Ile Glu Val Glu Lys Pro Phe Ala Ile Ala
200 205 210

aag gag tag agagcctggg ggacctcatc cctctaagca gctgtctgtg 788
Lys Glu
215

tggtgctcctgt caatccccac acagacgaag gtagccagtc acaaggttct gtgccaccct 848

ggccctagtg cttccatctg atgggggtgac cacaccctc acattccaca ggccctgattt 908

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aaaaaaaaa a 979

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Leu Ile Val Gly Ser Val Val Phe Leu Leu Leu Pro Gly Pro Ser Val
20 25 30

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Ala Asn Asp Lys Lys Lys Gly Pro Lys Val Thr Val Lys Val Tyr Phe
35 40 45

Asp Leu Gln Ile Gly Asp Glu Ser Val Gly Arg Val Val Phe Gly Leu
50 55 60

Phe Gly Lys Thr Val Pro Lys Thr Val Asp Asn Phe Val Ala Leu Ala
65 70 75 80

Thr Gly Glu Lys Gly Phe Gly Tyr Lys Asn Ser Lys Phe His Arg Val
85 90 95

Ile Lys Asp Phe Met Ile Gln Gly Gly Asp Phe Thr Arg Gly Asp Gly
100 105 110

Thr Gly Gly Lys Ser Ile Tyr Gly Glu Arg Phe Pro Asp Glu Asn Phe
115 120 125

Lys Leu Lys His Tyr Gly Pro Gly Trp Val Ser Met Ala Asn Ala Gly
130 135 140

Lys Asp Thr Asn Gly Ser Gln Phe Phe Ile Thr Thr Val Lys Thr Ser
145 150 155 160

Trp Leu Asp Gly Lys His Val Val Phe Gly Lys Val Leu Glu Gly Met
165 170 175

Asp Val Val Arg Lys Val Glu Ser Thr Lys Thr Asp Ser Arg Asp Lys
180 185 190

Pro Leu Lys Asp Val Ile Ile Val Asp Ser Gly Lys Ile Glu Val Glu
195 200 205

Lys Pro Phe Ala Ile Ala Lys Glu
210 215

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Met Leu Arg
1

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ctc tcc gaa cgc aac atg aag gtg ctc ctt gcc gcc gcc ctc atc gcg      226
Leu Ser Glu Arg Asn Met Lys Val Leu Leu Ala Ala Ala Leu Ile Ala
      5                      10                      15

ggg tcc gtc ttc ttc ctg ctg ctg ccg gga cct tct gcg gcc gat gag      274
Gly Ser Val Phe Phe Leu Leu Leu Pro Gly Pro Ser Ala Ala Asp Glu
20                      25                      30                      35

aag aag aag ggg ccc aaa gtc acc gtc aag gtg tat ttt gac cta cga      322
Lys Lys Lys Gly Pro Lys Val Thr Val Lys Val Tyr Phe Asp Leu Arg
      40                      45                      50

att gga gat gaa gat gta ggc cgg gtg atc ttt ggt ctc ttc gga aag      370
Ile Gly Asp Glu Asp Val Gly Arg Val Ile Phe Gly Leu Phe Gly Lys
      55                      60                      65

act gtt cca aaa aca gtg gat aat ttt gtg gcc tta gct aca gga gag      418
Thr Val Pro Lys Thr Val Asp Asn Phe Val Ala Leu Ala Thr Gly Glu
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aaa gga ttt ggc tac aaa aac agc aaa ttc cat cgt gta atc aag gac      466
Lys Gly Phe Gly Tyr Lys Asn Ser Lys Phe His Arg Val Ile Lys Asp
      85                      90                      95

ttc atg atc cag ggc gga gac ttc acc agg gga gat ggc aca gga gga      514
Phe Met Ile Gln Gly Gly Asp Phe Thr Arg Gly Asp Gly Thr Gly Gly
100                      105                      110                      115

aag agc atc tac ggt gag cgc ttc ccc gat gag aac ttc aaa ctg aag      562
Lys Ser Ile Tyr Gly Glu Arg Phe Pro Asp Glu Asn Phe Lys Leu Lys
      120                      125                      130

cac tac ggg cct ggc tgg gtg agc atg gcc aac gca ggc aaa gac acc      610
His Tyr Gly Pro Gly Trp Val Ser Met Ala Asn Ala Gly Lys Asp Thr
      135                      140                      145

aac ggc tcc cag ttc ttc atc acg aca gtc aag aca gcc tgg cta gat      658
Asn Gly Ser Gln Phe Phe Ile Thr Thr Val Lys Thr Ala Trp Leu Asp
      150                      155                      160

ggc aag cat gtg gtg ttt ggc aaa gtt cta gag ggc atg gag gtg gtg      706
Gly Lys His Val Val Phe Gly Lys Val Leu Glu Gly Met Glu Val Val
      165                      170                      175

cgg aag gtg gag agc acc aag aca gac agc cgg gat aaa ccc ctg aag      754
Arg Lys Val Glu Ser Thr Lys Thr Asp Ser Arg Asp Lys Pro Leu Lys
180                      185                      190                      195

gat gtg atc atc gca gac tgc ggc aag atc gag gtg gag aag ccc ttt      802
Asp Val Ile Ile Ala Asp Cys Gly Lys Ile Glu Val Glu Lys Pro Phe
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gcc atc gcc aag gag tag ggcacaggga catctttctt tgagtgaccg      850
Ala Ile Ala Lys Glu
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 35 40 45

Asp Leu Arg Ile Gly Asp Glu Asp Val Gly Arg Val Ile Phe Gly Leu
 50 55 60

Phe Gly Lys Thr Val Pro Lys Thr Val Asp Asn Phe Val Ala Leu Ala
 65 70 75 80

Thr Gly Glu Lys Gly Phe Gly Tyr Lys Asn Ser Lys Phe His Arg Val
 85 90 95

Ile Lys Asp Phe Met Ile Gln Gly Gly Asp Phe Thr Arg Gly Asp Gly
 100 105 110

Thr Gly Gly Lys Ser Ile Tyr Gly Glu Arg Phe Pro Asp Glu Asn Phe
 115 120 125

Lys Leu Lys His Tyr Gly Pro Gly Trp Val Ser Met Ala Asn Ala Gly
 130 135 140

Lys Asp Thr Asn Gly Ser Gln Phe Phe Ile Thr Thr Val Lys Thr Ala
 145 150 155 160

Trp Leu Asp Gly Lys His Val Val Phe Gly Lys Val Leu Glu Gly Met
 165 170 175

Glu Val Val Arg Lys Val Glu Ser Thr Lys Thr Asp Ser Arg Asp Lys
 180 185 190

Pro Leu Lys Asp Val Ile Ile Ala Asp Cys Gly Lys Ile Glu Val Glu
 195 200 205

Lys Pro Phe Ala Ile Ala Lys Glu
 210 215